

APPROVED		FIG.	
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FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGCTGCCGCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT
GGTGGACAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA
GGGCGACGGGTCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAAACCTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTGTCCTGACGGCTTCGAAGAAACG
GAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT
GCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTCAGAAGGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTA
AACAGACTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCA
TCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTTCGGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCAGGCTCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTTT

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FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEE
 KTLISKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTL
 KVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFS
 SLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPPCSAAQECK
 NANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGCADVDECSLAEKTCVRKNENCYN
 TPGSYVCVCPDGFEEETEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide: amino acids 1-24

N-glycosylation sites: amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites:

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 26-30

Casein kinase II phosphorylation sites:

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259,
 295-299, 339-343 and 349-353

Tyrosine kinase phosphorylation site: amino acids 303-310

N-myristoylation sites:

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164,
 164-170, 252-258 and 313-319

Aspartic acid and asparagine hydroxylation site: amino acids
 308-320

EGF-like domain cysteine pattern signature: amino acids
 166-178

Leucine zipper pattern: amino acids 94-116

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FIGURE 3

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAAGGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCCTGAGCAGCATGGCCCGGAGGAGCGCCTTC
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC
CGGGCCGCCGAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA
TAGGATTTGAAGAAGATATCCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCTTGGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA
TCAGTTGTTCAAGTTGGTTTTCCCATGTCTTGGAACAGGATGGGGTGGCAGCATTTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCCAAACACCTCAAAATGCTATCT
TCTTTAAACATGTCAACAAGCTGAGTGCCCGAGGCGGGTGCCGAAATGGAGGCTTTTGTAAT
GAAAGACGCATCTGCGAGTGTCTGATGGGTTCACGGACCTCACTGTGAGAAAGCCCTTTG
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACGTGACAAAGCAAACTGCTCAACCACCTGCTTTAATGGAGGGACC
TGTTTCTACCCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCCACAACCCTGTGAAATGGAGGTAAATGCATTGGTAAAGCAAATGTAAGTGTT
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACAT
GGAACCTGCCATGAACCCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAGGTACGAAGCCAGCCTCATACTATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC
ACACGCCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTTTAAGTTACACCAAGTTCATAGCCTTTGTAAACCTTTCA
TGTGTTGAATGTTCAAATAATGTTTCACTTAAAGTAACTGGCCTGAATTTTATTAGCT
TCATTATAAATCACTGAGCTGATATTTACTCTTCCTTTTAAGTTTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTTTCTTGTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA
TCAGGTTAAAATTTTTCAGTGTGTAGTTGGCAGATATTTTCAAATTACAATGCATTTATGGT
GTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAGATTTTATTGTGAGATATTTAGAT
GTTTGTTACATTTTTTAAAAATGCTCTTAATTTTTTAACTCTCAATACAATATATTTTGACC
TTACCATTATTCCAGAGATTGAGTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATT
AAACAATATAATATATTCTAAACACAATGAAATAGGGAATATAATGTATGAACTTTTTGCGAT
TGGCTTGAAGCAATATAATATATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTAT
ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

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FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094

><subunit 1 of 1, 379 aa, 0 stop

><MW: 41528, pI: 7.97, NX(S/T): 2

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGC
RNGGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCTFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW

Signal peptide: amino acids 1-28

N-glycosylation site: amino acids 88-92, 245-249

Casein kinase II phosphorylation site: amino acids 319-323

Tyrosine kinase phosphorylation site: amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature: amino acids

198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTTCGACAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG
 CCCCAGCCCACACCTTCACCAGGGCCCAGGAGCCACCATGTGGCGATGTCCAGTGGGGCTAC
 TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCCAGCAGGGTCGTGGGCGCCGG
 GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA
 GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT
 GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
 TGCCTCGGCGTGCCACCCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA
 TCCAGTCTTGGGAACGTACTGGGACAACGTGAACCGTTGCACCTGCCAGGAGAACAGGCAGT
 GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
 GAACCACAGCGCCTTCTGGGGCATGACCCTGGATTGAGGGCATTCGCTACCGCCTGGGCACCA
 TCCGCCCATCTTCTCGGTGATGAACATGCATGAAATTTATACAGTGCTGAACCCAGGGGAG
 GTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCTCTTGA
 CCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
 CAATCCATTCTCTGGGACACATGACGCCTGTCTGTGCCCCAGAACCTGCTGTCTTGTGAC
 ACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCTTGCCTCG
 CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC
 CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCC
 CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT
 CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
 TGGAGGTGCATGAGGACTTCTTCTTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
 CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
 AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCC
 CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGC GCGGCGTCAATGAGTGCGACATCGAG
 AGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCATCACTGAGGCTG
 CGGGCACCACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG
 GGGCGGTGACCCCAGCCTCGCCGACAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAAT
 CCCGGCGCGGGTTCCGCTGACGCAGCGCCCCGCTGGGAGCCGCGGGCAGGCGAGACTGGCG
 GAGCCCCCAGACCTCCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAG
 ATCCCAGGCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
 CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG
 TTGCCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACTCCGACTCCTGGGTTC
 AGTGACCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACCACACCTGGC
 TAATTTTTTGTATTTTTTGTAAAGAGGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAAC
 CCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTGCTGGGATTGCAGGCATGAGCC
 ACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTCTTTTCACTGTTTTAAAA
 TAAACCAAAGTATTGATAAAAAAAA

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FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC

ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNR

CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site: amino acids 78-82, 161-165

Casein kinase II phosphorylation site: amino acids 80-84,
117-121, 126-130, 169-173, 205-209, 296-300, 411-415

N-myristoylation site: amino acids 21-27, 39-45, 44-50,
104-110, 160-164, 224-230, 269-275, 378-384, 442-448

Amidation site: amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site:
amino acids 398-409

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FIGURE 7

AGGCTCCTTGGCCCTTTTCCACAGCAAGCTTNTGCNATCCCGATTTCGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCCTTTNGCCCCAGAACCTGCTGTCTTGTACA@CCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTCGGGGCAAGCGCCAGGCCACTGCCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCCTATAACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

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FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCAGCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAAGTGCCTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAAGATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCCTGGTTCCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCTCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTCTGTTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

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FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLLPPLRCSLHSACCSGDPASYRLWGAPLQPT
 LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPMPMALSRTPTTRQISSDT
 DPPADGPSNPLCCCFHGPFAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALR
 RAQ

Signal peptide: amino acids 1-47

N-glycosylation site: amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site: amino acids 22-26,
 76-80

N-myristoylation site: amino acids 56-60

Amidation site: amino acids 70-74

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FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHYQVVTGRRI
SATAEDGNKFACLIVETDTFGSRVRIKGAESEKYICMNKRGKLGKPSGKSKDCVFTEIVLE
NNYTAFQNRHEGWFMFAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide: amino acids 1-22

N-glycosylation site: amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 60-64

Casein kinase II phosphorylation site: amino acids 65-69

Tyrosine kinase phosphorylation site: amino acids 39-48,
89-97

N-myristoylation site: amino acids 69-75, 188-194

Amidation site: amino acids 58-62

HBGF/FGF family signature: amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
 GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
 CATA CGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCTCATCCAGT
 CATTTTGATTTTGCTGTTTATTTTTTTTTTTCTTTTTCTTTTTCCCACCACATTGTATTTTAT
 TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCCAGCCATGGGGCTTTTTCTCT
 GAAGTCTTGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAACTCCTGGCCTGCC
 CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
 CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAATTAATAATGC
 TGGATTTCCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
 AACTGGACGAATTCCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTTGCAGGAAAAC
 AATATTCAGACCATTTACGGGCTGCTCTTGCCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
 GGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGCTATTAGCC
 TCAAATTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCCCTGTGGAC
 TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCATATCCGACATGGCCTTCCAGAA
 TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG
 AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC
 CACCCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCAGAT
 AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
 ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC
 ACTGCTCGGAATAACCCTTGGTTTTGTGACTGCAGTATTAAATGGGTACAGAAATGGCTCAA
 ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCCTGAACAAGTCCGGG
 GGATGGCCGTCAGGGAATTAAATATGAATCTTTTGTCTGTCCCACCACGACCCCCGGCCTG
 CCTCTCTTACCCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTAT
 TCCAAACCCTAGCAGAAGCTACACGCCTCCAACCTCCTACCACATCGAACTTCCCACGATTC
 CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
 CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTACCGTGATGGCATA
 CAACTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTTCAGGAGCGCATAG
 TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
 TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAGAGGC
 CACCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
 CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
 GTGCTGGTGGTCTTGCTCAGCGTCTTTTGCTGGCATATGCACAAAAGGGGCGCTACACCTC
 CCAGAAGTGGAATACAACCGGGGCGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
 AGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTTTCAGATCGTCTCCTTAAATAACGAT
 CAACTCCTTAAAGGAGATTTTCAGACTGCAGCCCATTTACACCCCAAATGGGGGCATTAATTA
 CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC
 ACTGCCATACGTTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
 CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT
 TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG
 CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTTGTAACCTTTTGCTTTTTTAAATCTT

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FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
 EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLOENNIQTI
 SRAALAQLLKLEELHLLDDNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
 VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
 LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
 PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMARELNMNLLSCPTTTPGLPLFTP
 APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPISERIQLSIHFVND
 TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
 DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
 LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG
 DFRLQPIIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide: amino acids 1-42

Transmembrane domain: amino acids 542-561

N-glycosylation site: amino acids 202-206, 298-302, 433-437,
 521-525, 635-639, 649-653

Casein kinase II phosphorylation site: amino acids 204-208,
 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site: amino acids 319-328

N-myristoylation site: amino acids 2-8, 60-66, 149-155,
 213-219, 220-226, 294-300, 522-528, 545-551, 633-639

Amidation site: amino acids 581-585

Leucine zipper pattern: amino acids 164-186

Phospholipase A2 aspartic acid active site: amino acids 39-50

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FIGURE 14A

ACTTGGAGCAAGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCTCTCG
 CCTCCCACGAGCGATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGAEGAGG
 AAGACCCGGGTGGCTGCGCCCCCTGCCTCGCTTCCCAGGCGCCGGCGGCTGCAGCCTTGCCCC
 TCTTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCTGCTTTCTGCTGATCCTCGGACAG
 ATCGTCCTCCTCCCTGCCGAGGCCAGGGAGCGGTACGTGGGAGGTCCATCTCTAGGGGCAG
 ACACGCTCGGACCCACCCGCAGACGGCCCTTCTGGAGAGTTCCTGTGAGAACAAGCGGGCAG
 ACCTGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAG
 GAGTTCATCGTGGACATCTTGCAATTCTTGGACATTGGTCCTGATGTCACCCGAGTGGGCCT
 GCTCCAATATGGCAGCACTGTCAAGAATGAGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCG
 AGGTGGAGCGTGCTGTCAAGAGGATGCGGCATCTGTCCACGGGCACCATGACTGGGCTGGCC
 ATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCCGGCCCTGAGGGAGAA
 TGTGCCACGGGTGATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGG
 CTGCTAAGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTC
 AACACCTTGAAGTCCATTGGGAGTGAGCCCCATGAGGACCATGTCTTCCTTGTGGCCAATTT
 CAGCCAGATTGAGACGCTGACCTCCGTGTTCCAGAAGAAGTTGTGCACGGCCACATGTGCA
 GCACCCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTGGCTCATACTGTGCAGG
 TGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAAGATCCAGGATCTGTGTGC
 CATGGAGGACCACAACTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGT
 GCTACAGTGGCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCC
 TCAGAAAACCACGGATGTGAACATGAGTGTGTAAATGCTGATGGCTCCTACCTTTGCCAGTG
 CCATGAAGGATTTGCTCTTAACCCAGATGAAAAACGTGCACAAGGATCAACTACTGTGCAC
 TGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCTACTACTGCCGCTGC
 CACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGGACCACTGTGCACA
 GCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCCTTCGTCTGCCAGTGCT
 CAGAAGGCTTCCTCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCCTGCTG
 AGTGACCATGGTTGTGAATACTCCTGTGTCAACATGGACAGATCCTTTGCCTGTCAGTGTCC
 TGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTGCAAATTTGGACTCTTGTGCTCTGG
 GGGACCACGGTTGTGAACATTCGTGTGTAAGCAGTGAAGATTCGTTTGTGTGCCAGTGCTTT
 GAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTAT
 AGACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATAACGTGCGAGTGCTTGG
 AGGGATTCCGGCTCGCTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAAATCAACC

_____ To Figure 14B

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FIGURE 14B

_____ From Figure 14A

CACCATGGCTGCGAACACATTTGTGTTAATAATGGGAATTCCTACATCTGCAAATGCTCAGA
 GGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAATGCACTGAAGGCCCAATTGACC
 TGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGAGGTCTGGAAGCAG
 TTTGTCACTGGAATTATAGATTCCTTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCT
 CCAGTATTCCACACAGGTCCACACAGAGTTCCTCTGAGAACTTCAACTCAGCCAAAGACA
 TGA AAAAAGCCGTGGCCACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTG
 AAACACATGTTTGAGAGAAGTTTTACCCAAGGAGAAGGGGCCAGGCCCTTTCCACAAGGGT
 GCCCAGAGCAGCCATTGTGTTACCGACGGACGGGCTCAGGATGACGTCTCCGAGTGGGCCA
 GTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTGAGGAG
 GAACTACAAGAGATTGCCTCTGAGCCACAAACAAGCATCTCTTCTATGCCGAAGACTTCAG
 CACAATGGATGAGATAAGTGA AAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCG
 ATGGAAGACAGGACTCTCCAGCAGGGGAACTGCCAAAAACGGTCCAACAGCCAACAGAATCT
 GAGCCAGTCACCATAAATATCCAAGACCTACTTTCTGTTCTAATTTTGCAGTGCAACACAG
 ATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTTCCCATTC AACAAAAC
 CTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGTTC
 CAGAACCTTGCAAACGAAGAAGTAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAG
 AATGGAAGCCCTGGAAAATCGCCTGAGATACAGATTGAAGATTAGAAATCGCGACACATTTGT
 AGTCATTGTATCACGGATTACAATGAACGCAGTGCAGAGCCCCAAAGCTCAGGCTATTGTTA
 AATCAATAATGTTGTGAAGTAAACAATCAGTACTGAGAAACCTGGTTTGCCACAGAACAAA
 GACAAGAAGTATACACTAACTTGTATAAATTTATCTAGGAAAAAAATCCTTCAGAATTCTAA
 GATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAATATACTGTGGACA
 CAACTTGCTTCTGCCTCATCCTGCCTTAGTGTGCAATCTCATTGACTATACGATAAAGTTT
 GCACAGTCTTACTTCTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTTGTACTGGACTTT
 ACCTTGATATATGTATATGGATGTATGCATAAAATCATAGGACATATGTACTTGTGGAACAA
 GTTGGATTTTTTATACAATATTAAAATTCACCACTTCAG

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FIGURE 15

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFHI
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KRMRLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSTVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGC
EHECVNMEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGLI
NEDLKTC SRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTC AKLDSCALGDHGCE
HSCVSSDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLA
EDGKRCRRKDVCCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQEGGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALEDS DGRQDS
PAGELPKTVQQPTESEPTVINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide: amino acids 1-23

N-glycosylation site: amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site: amino acids 49-53,
118-122, 149-153, 176-180, 223-227, 243-247, 401-405, 442-446,
501-505, 624-628, 673-677, 706-710, 780-784, 781-785, 819-823,
866-870

N-myristoylation site: amino acids 133-139, 258-264, 299-305,
340-346, 453-459, 494-500, 639-645, 690-696, 752-758, 792-798

Amidation site: amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site: amino acids
253-265, 294-306, 335-347, 376-388, 417-423, 458-464, 540-546,
581-587

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FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CCATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTTGTTCCCTGGGGCTGA
GTGCCCTCGCGCCCCCCTCGCGGGGCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCTGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAAGCTGGCTCTCTGGTATTGATGAC
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCCTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAA
TGTTTGTATGAAAAA

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FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
 SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLOEKDSGPY
 SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQ
 WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
 VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLTPWPKSSDTISKNGTL
 SSVTSARALRPPHGPFRPGALTPTPSLSSQALPSRLPTTDGAHPQPISPIPGGVSSSSGLSR
 MGAVPVMVPAQSQAAGSLV

Signal peptide: amino acids 1-29

Transmembrane domain: amino acids 245-267

N-glycosylation site: amino acids 108-112, 169-173, 213-217,
 236-240, 307-311

N-myristoylation site: amino acids 90-96, 167-173, 220-226,
 231-237, 252-258, 256-262, 262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 164-175

FIGURE 18

[illegible]

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FIGURE 19

MKRLPLLVFSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENTVNANCHLDNVCTAA
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIITYIEILAESSSLLGYKNNTISAKDTL
SNSTLTEFVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFQKTTEFDT
NSTDIALKVFFFDSDYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVAVAFLYYKSI GPLLS
SSDNFLLKPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTD RYRSLCAF
WNYSPTMNGSWSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIIAGL
LHYFFLAFAWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFS AALGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLHVHVASVVTAYLFTVSNAFQGMFI FLFCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide: amino acids 1-19

Transmembrane domain: amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636, 648-664

N-glycosylation site: amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181, 188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site: amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 360-364

Casein kinase II phosphorylation site: amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154, 155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329, 346-350, 608-612

Tyrosine kinase phosphorylation site: amino acids 36-44, 669-677, 670-678

N-myristoylation site: amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394, 434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site: amino acids 75-87

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FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA
GGAGTCTATGTGGCATTTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

APPROVED	FIG. 21	
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FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
 CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCC GGCTGGGA
 CAAGAAGCCGCCGCTGCTGCCCGGGCCCGGGGAGGGGGGCTGGGGCTGGGGCCGGAGGCGG
 GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
 TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCGGAG
 CCGCCGCGCCGTGAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
 GGCACCTACAGCCCCGCAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCGG
 AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG
 ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC
 CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC
 ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCGTGGACTGCGCGCGGGGC
 CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGCCCATCAAGGG
 CGTGACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGGCTGCTTCAGT
 ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
 TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
 CAGAGGCTTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG
 AGGACCTCAGGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCCCTGGAGACCGACAGCATG
 GACCCATTTGGGCTTGTACCCGGAAGTGGAGGCGGTGAGGAGTCCCAGCTTTGAGAAGTAACT
 GAGACCATGCCCGGGCCTCTTCACTGCTGCCAGGGGGCTGTGGTACCTGCAGCGTGGGGGACG
 TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
 GTTGATACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
 CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCCTGGGCCCCCATTTCTGCTCCCTCGA
 GGTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
 TCACTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC
 CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTAGGAACAGGTGATCCACTCTGTA
 AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
 ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCACCAG
 GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAATTCCCC
 CTGAGGCCAGTTCTGTGATGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTCACCTGC
 TTCCATCTCCCAGCCCACCAGCCCTCTGCCCACCTCACATGCCTCCCCATGGATTGGGGCCT
 CCCAGGCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT
 TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
 CCTTTCCCCAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA
 TCTCTTATTTTCTTACATTATTTATGCCCCCAAATTATTTATGTATGTAAGTGAGGTTTG
 TTTTGTATATTAAAATGGAGTTTGTTTGT

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FIGURE 22

M R S G C V V V H V W I L A G L W L A V A G R P L A F S D A G P H V H Y G W G D P I R L R H L Y T S G P H G L S S C F L R I
R A D G V V D C A R G Q S A H S L L E I K A V A L R T V A I K G V H S V R Y L C M G A D G K M Q G L L Q Y S E E D C A F E E
E I R P D G Y N V Y R S E K H R L P V S L S S A K Q R Q L Y K N R G F L P L S H F L P M L P M V P E E P E D L R G H L E S D
M F S S P L E T D S M D P F G L V T G L E A V R S P S F E K

Signal peptide: amino acids 1-22

Casein kinase II phosphorylation site: amino acids 78-82,
116-120, 190-194, 204-208

N-myristoylation site: amino acids 15-21, 54-60, 66-72,
201-207

Prokaryotic membrane lipoprotein lipid attachment site: amino
acids 48-59

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FIGURE 23

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGCCGCCACCGCCTCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA
AGAAGACTGTTTCCTCCAGATTAGAGTGGAAGAACTGGGTCCGAGTGTCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAAACTGGAAGT
CTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTC
TGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATCTTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGG
CCGCGGCGGGCGGATCACGAGGTCAGGAGTTCAGACCAGTCTGGCCAATATGGTGAAACCC
CATCTCTACTAAAATACAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAAATAAATA
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

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FIGURE 24

MARRSRHRLLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
 WKKLGRSVSFVYYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGONLEED
 TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST
 NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN SVGYRRC PGKRMQVDDL NISGIIAAVVVVA
 LVISVCGLGVCYAQRKGYFSKETS FQKSNSSSKATTMSENVQWLTPVIPALWKAAAGGSRGO
 EF

Signal peptide: amino acids 1-20

Transmembrane domain: amino acids 130-144, 238-258

N-glycosylation site: amino acids 98-102, 187-191, 236-240,
 277-281

Casein kinase II phosphorylation site: amino acids 39-43,
 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site: amino acids 182-188, 239-245, 255-261,
 257-263, 305-311

Amidation site: amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
 AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCCGACCCTGGCAT
 CATGCTGCTATTCTTGCAAATACTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA
 ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA
 TTATATCATTAAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTTGGACAATG
 CAATTGTGGCACTGGCACTTATTTTCAGTGAAGAAAACTTTGTGGTTCTATGGCATTCATCA
 TTTGACAAATGCAAGCATCTTCCTTATCAATCAGCTCCTATTGAACCTTACTAGCACTGACTG
 TGGAAATCCTTAAGGGCCCATTAACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
 CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
 TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTTAT
 ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCCAGCCAGATTGCC
 AGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAG
 ACTTTCCAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAAT
 ATTAATGTAAAAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAACAACTTACTGA
 ACTGCCTGAAAAATGTCTGTCCGAACCTGAGCAACTTACAAGAACTCTATATTAATCACAAC
 TGCTTTCTACAATTTACCTGGAGCCTTTATTGGCCTACATAATCTTCTTCGACTTCATCTC
 AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAGAGAT
 TCTGATGATTGGGGAAAAATCCAATTATCAGAATCAAAGACATGAACTTTAAGCCTCTTATCA
 ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTT
 GGACTGGAAAACTTAGAAAGCATCTCTTTTTACGATAACAGGCTTATTAAAGTACCCCATGT
 TGCTCTTCAAAAAGTTGTAAATCTCAAATTTTTGGATCTAAATAAAAAATCCTATTAATAGAA
 TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAAGAGTTGGGGATAAATAATATGCCT
 GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC
 TACTAACAAACCCTAGATTGTCTTACATTACCCCAATGCATTTTTTCAGACTCCCCAAGCTGG
 AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG
 CCAAACCTCAAGGAAATCAGCATAACAGTAACCCCATCAGGTGTGACTGTGTCTATCCGTTG
 GATGAACATGAACAAAACCAACATTTCGATTTCATGGAGCCAGATTCAGTGTTCGCGTGGACC
 CACCTGAATTCCAAGGTCAGAATGTTGGGCAAGTGCATTTTCAGGGACATGATGGAAATTTGT
 CTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT
 TTCTTTTCACTGTAGAGCTACTGCAGAACCCAGCCTGAAATCTACTGGATAACACCTTCTG
 GTCAAAAACCTCTTGCCATAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA
 GATATAAATGGCGTAACCTCCCAAAGAAGGGGGTTTATATACTTGTATAGCAACTAACCTAGT
 TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG
 GCTCTTTGAATATTAAAATAAGAGATATTCAGGCCAATTCAGTTTTGGTGTCTCTGGAAAGCA
 AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTTGTCAAGACTGAAAATTCTCA
 TGCTGCGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
 CATCAACTGAGTATAAAATTTGTATTGATATTTCCACCATCTATCAGAAAAACAGAAAAAAA
 TGTGTAAATGTCACCACCAAAGGTTTGCACCCTGATCAAAAAGAGTATGAAAAGAATAATAC
 CACAACACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA
 GCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
 AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA
 AGAAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTT
AAAAACCAAGGAAACCTACTCCAAAAATGAAC

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FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
 FPARLPANTQIILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQELSVYLE
 ENKLTPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDA
 LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRL
 IKVPHVALQKVVNLKFLDLNKNPINRIRRGDFSMLHLKELGINNMPELISIDSLAVDNLPD
 LRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISIHSPNIRC
 DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGNVRQVHFRDMMEICLPLIAPESFPSNLNV
 EAGSYVSFHCRTAEAPQPEIYWITPSGQKLLPNTLTDFYVHSEGLDINGVTPKEGGLYTC
 IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFFV
 KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
 YEKNNTTTLMACLGGLLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPPLIN
 LWAGKEKSTSLKVKATVIGLPTNMS

Signal sequence: amino acids 1-22

Transmembrane domain: amino acids 633-650

N-glycosylation site: amino acids 93-97, 103-107, 223-227,
 382-386, 522-526, 579-583, 608-612, 624-628, 625-629

Casein kinase II phosphorylation site: amino acids 51-55,
 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site: amino acids 570-579

N-myristoylation site: amino acids 13-19, 96-102, 158-164,
 221-227, 352-358, 437-443, 491-497, 492-498, 634-640, 702-708

Cell attachment sequence: amino acids 277-280

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FIGURE 27

GCCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTA
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTTGGCTGGTTCACCTATGGTGATCTCATATGTGGTATATTATGTGAGGCCAAAATCAGGAG
GATGCCCCGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTTTCGATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA
ACTTTGTATTTTCAGTTTTTTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACA
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT
AATTTAAAAGCAAATAAAAGCTTAACCTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAA
ACA

APPROVED	FIG.	
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FIGURE 28

MNLVDLWLTRSLSMCLLLQS FVLMILCFHSASMCPKGCLCSSSGGLNVTCSNANLKEIPRDL
 PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLSDNR
 IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL
 NAANDADLCNLPKKT TDYAMLVTMFGWFTMVISYVYYYVRQNQEDARRHLEYLKS LPSRQKK
 ADEPDDISTVV

Signal sequence: amino acids 1-33

Transmembrane domain: amino acids 205-220

N-glycosylation site: amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 amino acids 199-203

Casein kinase II phosphorylation site: amino acids 162-166,
 175-179

N-myristoylation site: amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT
GGGCTCAGTGCTGTGTCAGGCTCGGCCACGGGCTGCCCCGCCCCGCTGCGAGTGCTCCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGGCG
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGAT
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCCTAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGCACGGCCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC
TGCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTTCCTCAACCTCTCCTACAACCCCATCA
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGCTCAA
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCCTGTGGGTGTTCCGG
CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCCGAGTTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCACTACTTCACCTGCCGCCGCG
CCCGCATCCGGGACCGCAAGGCCCAGCAGGTGTTTGTGGACGAGGGCCACACGGTGCAGTTT
GTGTGCCGGGGCCGATGGCGACCCGCCGCCCATCCTCTGGCTCTCACCCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGAC
TCCATGCCCCGCCACCTGCATGTGCGCAGCTACTCGCCCGACTGGCCCCATCAGCCCAACAA
GACCTTCGCTTTCATCTCCAACCAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG
TGCCTTTCCCCTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC
CTGGGCGTCGTCTTCTGCCTGGTGCTGCTGTTTCTCTGGAGCCGGGGGCAAGGGCAACAC
AAAGCACAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
ACGCGCCCCGCAAGTTCAACATGAAGATGATATTGAGGCGGGGCGGGGGGAGGGACCCCCG
GGCGGCCGGGCAGGGGAAGGGGCTGGTGCACCTGCTCACTCTCCAGTCCTTCCCACCTC
CTCCCTACCCTTCTACACACGTTCTCTTCTCCCTCCCGCCTCCGTCCCCTGCTGCCCCCG
CCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCAGACCTGGGGACCCCA
CCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACTTTCTCTGTAACCTGGGTTTCAATAATTATGGATTTT
TATGAAAACCTTGAAATAATAAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

APPROVED	G. FIG.	
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FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNERTL
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTREALSHLHGLIVLRRLRLNINAI RDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRLNLSYNPISTIEGSMLEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSGVGNLETLILDSNPLA
CDCRLLWVFRRRWRLNFRNQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVPDGTLEVRYAQVQDNGTYL
CIAANAGGND SMPAHLHVSYS PDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGN TKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence: amino acids 1-41

Transmembrane domain: amino acids 556-578

N-glycosylation site: amino acids 144-148, 202-206, 264-268,
274-278, 293-297, 341-345, 492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site: amino acids 49-53,
108-112, 146-150, 300-304, 348-352, 349-353, 607-611

Tyrosine kinase phosphorylation site: amino acids 590-598

N-myristoylation site: amino acids 10-16, 32-38, 37-43,
113-119, 125-131, 137-143, 262-268, 320-326, 344-350, 359-365,
493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site: amino
acids 32-43

APPROVED	C. FIG.	
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FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC
ATCGTAGTCCACCCCCCTCCCCATCCCCAGCCCCCGGGGATTTCAGGCTCGCCAGCGGCCAGCC
AGGGAGCCGGCCGGGAAGCGCGGATGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGC
TGTTTCGCCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAGA
GAGCCCTTCGAGATAATCGAATTTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAG
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTTCCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACCCCAGTCCGGTGCCCT
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCCTGCTG
CTCATCATGCTCATCTTCCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTATCTAGAGGCGCCTGCCCACTTCCTGC
GCCCCCAGGGGCCCTGTGGGGACTGCTGGGGCCGTACCAACCCGGACTTGTTACAGAGCAA
CCGCAGGGCCGCCCTCCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTTGTACTCGGTTTGGAATGGGGAGGGAGGAGGGCGGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTTCGTGGCTTCTCTGCATTTGGGTTATTATTATTTTGTAAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAACA
AACAAAAACA

APPROVED	C.G. FIG.	
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FIGURE 32

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLCQVKDHEDSSLQW
 SNPAQQTLYFGEKRALRDNRILQVLTSTPHELSSISNVALADEGEYTCSIFTMPVRTAKSLV
 TVLGIPQKPITITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
 TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
 KLLHCEGRGNPVPQQYLWEKEGSVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
 YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLI FLGHYLRHKGTYLTAEAKGSDD
 APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence: amino acids 1-20

Transmembrane domain: amino acids 331-352

N-glycosylation site: amino acids 25-29, 290-294

Casein kinase II phosphorylation site: amino acids 27-31,
 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site: amino acids 2-8, 23-29, 156-162,
 218-224, 295-301, 298-304, 306-310, 334-340, 360-364, 385-389,
 386-390

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCTTTTCTTCTCCTTTTCCTGG
 CTTTCGGACATTGGAGCACTAAATGAACTTGAATTGTGTCTGTGGCGAGCAGGATGGTTCGCTG
 TTACTTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT
 GCTGGAGACGTCTCTTTGTTTTGCCGCTGGAAACGTTACAGGGGACGTTTGCAAAGAGAAGA
 TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA
 AGTCTGCAGCGTTTCACTGCCCCGACTTCCCAGTTTTTACCATTTATTTCTGCAATGGCAATTC
 CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGG
 AAAACAATGGCTTGCATGAAATCGTTCCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGG
 CTGCACATCAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
 TCTGGAATATCTCCAGGCTGATTTTAAATTTATTACGAGATATAGACCCGGGGGCTTCCAGG
 ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTTACCTGCCAAC
 GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC
 CTATGAGGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTT
 GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCCAAGAATGCC
 CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
 CACCGAACAGGACTTGTGTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGGCGCCCCCTG
 CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAAGAG
 GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
 CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCTTAGCTAACA
 GTTTACCCTGCCCTGGGGGCTGCAGCTGCGACCACATCCAGGGTCGGGTTTAAAGATGAAC
 TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA
 GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA
 ACCTCATTTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACTTTCAAG
 AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA
 GAAATTCGCGGGGCTGCAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
 TCCTCCCGGGCACTTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAACAACCTG
 CTGAGGTCCCTGCCTGTGGACGTGTTGCTGGGGTCTCGCTCTCTAAACTCAGCTGCACAA
 CAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA
 TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCA
 GAACGCTTGGGTTCGGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTCTT
 TAGAAAGGATTTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
 CGCCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTGGCGGAGACCGGGACGCACTCC
 AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT
 GTTTGTACCTCCGCCTTACCCTGGTGGGCATGCTCGTGTTTATCCTGAGGAACCGAAAGC
 GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCTACAGACAGTCTGT
 GACTCTTCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG
 TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCG
 ATACATCCTTCCCCACCGCAGGCACCCCGGGGGCTGGAGGGGCGTGTACCCAAATCCCCGCG
 CCATCAGCCTGGATGGGCATAAGTAGATAAAATAACTGTGAGCTCGCACAACCGAAAGGGCCT
 GACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
 GCCAGCTCGCTCTTTGCTGAGAGCCCCCTTTTGACAGAAAGCCAGCACGACCCTGCTGGAAG
 AACTGACAGTGCCCTCGCCCTCGGCCCCGGGGCCTGTGGGGTTGGATGCCGCGGTTCTATAC
 ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTTCCCTGTGGATTAG
 CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT
 TGTAATAAGTAACTTTGACTTCTGAC

APP'D	FIG.	
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FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
 LFLHGNSLTRLFPNEFANFYNAVSLHMENGLHEIVPGAFLGLQLVKRLHINNKKIKSFRKO
 TFLGLDDLEYLQADFNLLRDIDPGAQDLNKLEVLILNDNLISTLPANVFQYVPITHLDLRG
 NRLKTLPEYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
 GKDLNETTEQDLCPKLRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTK
 IPGNWQIKIRPTAAIATGSSRNKPLANSPLCPGGCSCDHIPGSGLKMNCCNNRVSSSLADEKP
 KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY
 LDTLSREKFAGLQNLEYLNVEYNAIQILILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
 SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSTIVPFKQWAERLGSEVLMSDLKC
 ETPVNFRRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
 VPGLLLVFVTSFTVVGMLVFILNRNRKRSKRDRANDSSASEINSLQTVCDSSYWHNGPYNADG
 AHRVYDCGSHSLSD

Signal sequence: amino acids 1-15

Transmembrane domain: amino acids 618-638

N-glycosylation site: amino acids 18-22, 253-257, 363-367,
416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 122-126, 646-650

Casein kinase II phosphorylation site: amino acids 30-34,
180-184, 222-226, 256-260, 366-370, 573-577, 608-612, 657-661,
666-670, 693-697

N-myristoylation site: amino acids 17-23, 67-73, 100-106,
302-308, 328-334, 343-349, 354-360, 465-471, 493-499, 598-604,
603-609

Prokaryotic membrane lipoprotein lipid attachment site: amino
acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCCCTGACCCCAGAATAACTCAGGGC
 TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAACTGTTGGC
 CGCTGGGCCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGG
 AAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
 AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCGGGGCCTCAG
 AGAATGAGGCCCGGCGTTTCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCGGGGCGG
 CGGCGAACACCCCCACTGCCGACCGTGCTGGCTGCTCGGCCTCGGGGGCCTGCTACAGCCTGC
 ACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC
 AGCACCGTGCGTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCCAGG
 GCCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCCACT
 GCACCCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCTCCGACCCCGGCGGTCTC
 GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGC
 GGTACTCCAGGCCACCGGTGGGGTTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
 GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCCTGCGCCGCGCCCCGGG
 GCCGCCTCTAACTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
 TCCACCTGGGACCGAGGTGAGTGCGCTCTGCCGGGGACAGCTCCCGATCTCAGTTACTTGCA
 TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTGCCCC
 GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG
 CTTTGCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCA
 GTGGGGAAGGACAGCCGACCCTTGGGGGGACCGGGGTGCCACCAGGCGCCCGCCGGCCACT
 GCAACCAGCCCCGTGCCGAGAGAACATGGCCAATCAGGGTTCGACGAGAAGCTGGGAGAGAC
 ACCACTTGTCCCTGAACAAGACAATTCAGTAACATCTATTCCTGAGATTCTTCGATGGGGAT
 CACAGAGCACGATGTCTACCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC
 CCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTTT
 CGACTCCTCCTCTGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTTGGTGATCT
 TGACCATGACAGTACTGGGGCTTGTCAGCTCTGCTTTCACGAAAGCCCCTCTTCCCAGCCA
 AGGAAGGAGTCTATGGGCCCCGCCGGGCCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC
 CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAG
 CAGAGGGTGCTTGCTGGCGGAGTCCCCTCTTGCTCTAGTGATGCATAGGGAAACAGGGGA
 CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGGAACCAAGAGGAACTTAC
 TTGTGTAAGTACAAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTACTCCACTGAG
 GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCCTTTAGGA
 TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTTCGGAGAA
 TTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATATAATTTACA
 TTAATAATAATTTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTTCAGGCTAGGAGTAT
 ATTGGTTTCGAAATCCCAGGGAAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

APPROVED	O.C. FIG.	
BY	CLASS	SUBCLASS
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FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAE LRAVLALLRAGPGPGGGS KDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCTIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence: amino acids 1-16

Transmembrane domain: amino acids 399-418

N-glycosylation site: amino acids 189-193, 381-385

Glycosaminoglycan attachment site: amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 98-102, 434-438

Casein kinase II phosphorylation site: amino acids 275-279,
288-292, 342-346, 445-449

N-myristoylation site: amino acids 30-36, 35-41, 58-64,
59-65, 121-127, 151-157, 185-191, 209-215, 267-273, 350-356,
374-380, 453-459, 463-469, 477-483

Aspartic acid and asparagine hydroxylation site: amino acids
262-274

APPROVED	O.G. FIG.	
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DRAFTSMAN		

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FIGURE 37

CGGACGCGTGGGATTTCAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCCGCGTATC
CCCCGGCTACCTGGGCGCGCCCGCGGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGTGCCGGCGCGCGCGCCGTGGGGTGCAAACCCCGAGCGTCTACGCTGCCATGA
GGGGCGGAACGCCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGTTTTCTGGAGTGTACCCTCCAAATAGCAAATGTACTTGGAATCA
CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTCATAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCG
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAC
CCCCAACTGGCCAGACCGGGATTACCCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTTAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACTTCTTATTCAGT
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTCAGGCCAAAA
AACTGCCTACAACACAGAACAGCCTGTCACCACCACATTCCCTGTAACCACGGGTTTAA
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTTCAGCAGGCGGG
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG
TTAACAGTGAAGTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTCT
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT
TGCTGCTGTGAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAGCGTTTATTTATACATCTCTGTAAAAGGAT
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTTTAGAAGTGCAATATTTATAGT
GTTATTTGTTTCACCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCCTTTTCTA
AATCAATGCTTAATAAAATATTTTTAAAGGAAAAA

APPROVED	D.C. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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FIGURE 38

M R G A N A W A P L C L L L A A A T Q L S R Q Q S P E R P V F T C G G I L T G E S G F I G S E G F P G V Y P P N S K C T W K
I T V P E G K V V V L N F R F I D L E S D N L C R Y D F V D V Y N G H A N G Q R I G R F C G T F R P G A L V S S G N K M M V
Q M I S D A N T A G N G F M A M F S A A E P N E R G D Q Y C G G L L D R P S G S F K T P N W P D R D Y P A G V T C V W H I V
A P K N Q L I E L K F E K F D V E R D N Y C R Y D Y V A V F N G G E V N D A R R I G K Y C G D S P P A P I V S E R N E L L I
Q F L S D L S L T A D G F I G H Y I F R P K K L P T T T E Q P V T T T F P V T T G L K P T V A L C Q Q K C R R T G T L E G N
Y C S S D F V L A G T V I T T I T R D G S L H A T V S I I N I Y K E G N L A I Q Q A G K N M S A R L T V V C K Q C P L L R R
G L N Y I I M G Q V G E D G R G K I M P N S F I M M F K T K N Q K L L D A L K N K Q C

Signal sequence: amino acids 1-23

N-glycosylation site: amino acids 355-359

Casein kinase II phosphorylation site: amino acids 64-68,
142-146, 274-278

Tyrosine kinase phosphorylation site: amino acids 199-208

N-myristoylation site: amino acids 34-40, 35-41, 100-106,
113-119, 218-224, 289-295, 305-311, 309-315, 320-326, 330-336

Cell attachment sequence: amino acids 149-152

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FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCCCACGGCGCCCCGCGGGCTGGGGCGGTTCGCTTCTT
 CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGGCCCCATGGCCCCCGAAGG
 GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCCTCAACCTCCCAGGACCTATCTGG
 CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTCATACCTG
 CCGGGGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACFTTGGAG
 GTGGAAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTG
 GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
 GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCACAAGCAGCAGGAGGCCCCGGACCTCTTCC
 AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGCCCTCCTGC
 CTTCCCTGTCCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
 GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
 AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT
 TTTGGCCCCCTGTGCCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGG
 CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT
 GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
 GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA
 GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
 ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
 ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
 AGAAGACGAGTTGGTGGTGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
 CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
 ACTGGCTACTGGTTGTGAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATTA
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCCCAGAGCTTGGGCTGCCC
 TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTG
 CCTTACAGAGCAGCCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
 CCTGAAGGTGGATACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
 ATTTCAAAGTTTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG
 GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT
 TCTGTGTTACACATCCCCACACCCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA
 AAGGTCTTGAAAGTTAAAAAAAAAAAAAAAAAAAAAAAAA

APPROVED	G.G. FIG.	
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FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQSPPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDCQAG
YGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGP EESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCS PGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDLVVLQOMFFG
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGF IKG R

Signal sequence: amino acids 1-29

Transmembrane domain: amino acids 372-395

N-glycosylation site: amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 290-294

Casein kinase II phosphorylation site: amino acids 63-67,
73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site: amino acids 8-14, 51-57, 59-65, 69-75,
70-76, 167-173, 173-179, 177-183, 188-194, 250-256, 253-259,
267-273, 280-286, 283-289, 326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site: amino acids
321-333

EGF-like domain cysteine pattern signature: amino acids
181-193

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FIGURE 41

TGAGACCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
 GCACCATGCAGCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCCCTGGCCAGCCCCGGG
 CCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT
 GCCCACCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCCAGT
 ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTTCAGCCAGAGC
 TTCCGAGAGGTGGCCGGCAGGTTCCCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG
 CATGGAGCAGCGGCTGCCGCCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG
 AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGCGCCCCGGGCC
 CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA
 CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
 ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
 GAGCATCTGGGCCCGCTGGCGTCCGGCGCCCACAAGCTGGTCCGCTTTGCCTCGCAGGGGGC
 GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTGGACCTTGGGGACTATGGAG
 CTCAGGGCGACTGTGACCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
 ATGTACATTGACCTGCAGGGGATGAAGTGGGCGGAGAACTGGGTGCTGGAGCCCCCGGGCTT
 CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTTCAAGTGGC
 CGTTTCTGGGGCCTCGACAGTGCATCGCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC
 ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCCAACATGAGGGTGCAGAA
 GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCATAGGCGCCTAGTG
 TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTCGAGGGTACCAGGAGAGCTG
 GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT
 CCTCTGACAAGTTACCTCACCTAATTTTTGCTTCTCAGGAATGAGAATCTTTGGCCACTGGA
 GAGCCCTTGCTCAGTTTTCTCTATTCTTATTATTCACTGCACTATATTCTAAGCACTTACAT
 GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCCANTGTGTCATTGTTTACTTGTCTGTAC
 TGGATCTGGGCTAAAGTCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT
 TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAACATGAATAAAACACATTTTATTCT
 AAAA

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FIGURE 42

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
 ALLQRSHGDRSRGKRFSQS FREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
 VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRVSVHESGWKAFDVTAEVNF
 WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLTLGDYGAQ
 GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPPEAFAFKWPF
 LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKSCASDGALVPRRLQP

Signal sequence: amino acids 1-18

N-glycosylation site: amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 amino acids 76-80

Casein kinase II phosphorylation site: amino acids 68-72,
 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site: amino acids 19-25, 156-162, 225-231,
 260-266, 274-280

Amidation site: amino acids 74-78

TGF-beta family signature: amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGACAAA
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCTCTGCCACCATTTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCT
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGTCATCGTGGCAGCCGTCTTGTAACCCTGATTCTCCTGGGAAT
CTTGTTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTCTGGTGTGAGCCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTTCACAGGATGCCTTATTTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTTCCTACCACTGCTGAGTGGCCTGGAACCTTGTTTAA
GTGTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGGTCGCAGGAATCTGCACTCAACTGCCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG
TGATGACACTGGGGTCCCTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG
GATTTAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCGGGAGTTCGGGATCAGCCTGACCA
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

APPROVED	C.R. FIG.	
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DRAFTSMAN		

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FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSLAYSGFSSPRVEW
KFDQGDTRRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYSRRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence: amino acids 1-27

Transmembrane domain: amino acids 238-255

N-glycosylation site: amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 270-274

Casein kinase II phosphorylation site: amino acids 34-38,
82-86, 100-104, 118-122, 152-156, 154-158, 193-197, 203-207,
287-291

N-myristoylation site: amino acids 105-111, 116-122, 158-164,
219-225, 237-243, 256-262

APPROVED	FIG. FIG.	
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FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
CGGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCCGCTTTCCACCCGACCTCTGCCCAGGCCGCGAGGCCCGAGCTCAG
GCTCGTGCCACCCACCAAGTTCCAGTGCCGCACCAGTGGCTTATGCGTGCCCGCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCCCTGCACCGGCGTCA
GTGACTGCTCTGGGGGAAGTACAAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGAC
CTCGCTGCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

APPROV	AC. FIG.	
BY	CLASS	SUBCLASS
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FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
 TSGLCVPLTWRCRDLDCSDGSDEEEECRIEPTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL
 RNC SRLACLAGELRCTLSDDCIPLTWRC DGHPCPDSSDELGCGTNEILPEGDATTMGPPVT
 LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLV TATLL
 LLSWLRAQERLRPLGLLVAMKESLLLSEQKTS LP

Signal sequence: amino acids 1-30

Transmembrane domain: amino acids 230-246

N-glycosylation site: amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site: amino acids 84-88,
 140-144, 161-165, 218-222

N-myristoylation site: amino acids 3-9, 10-16, 26-32, 30-36,
 112-118, 166-172, 212-218, 224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 44-55

Leucine zipper pattern: amino acids 17-39

APPROVED	FIG. FIG.	
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FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG
 GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCGACAGA
 CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
 GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
 GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
 CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
 GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
 GCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGA
 TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA
 ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTTCATGAAGGATTCAAGATCCGG
 TACCCCGACCTACACAATATGGTTTCATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
 CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
 TCCAGACCTCCTTCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTT
 GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCCGGTG
 CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTTCGTCT
 GCCACCCGCGGCCTTGTGAGCGCTACAACCACGGAACGTGGTGAGTTTTACTGCGATCCT
 GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTTCTTC
 TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCCCTCCTGA
 CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGCTGCTGCTCGTCATC
 CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAG
 TTCCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG
 ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGGTACATGGCCTCTGTGGGCCAG
 GGCTGCCCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA
 CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA
 GTCTGTATTACCTCCCAGGTGCCAAGAGAGACCCACCCTGCTTCGGACAACCCTGACATA
 ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCCACTGGGT
 GTTGTTCCTAAGAAACTGATTGATTAAAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAA
 ATACATGTTGATCTGTGGAGTTGATTCCTTTCTTCTCTTGGTTTTAGACAAATGTAAACAA
 AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC
 CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAAAGNAAAAA

APPROVED	G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
 PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
 PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRELAS
 SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP
 PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
 WPSTHETLLTTWKIVAFTATSVLLLVLLLVILARMFQTKFAHFPPRGPPRSSSSDPDEFVVD
 GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPDDQSPPAYPGSGD TDTGPGESETCDS
 VSGSSELLQSLYSPPRCQESTHPASDNPDI IASTAEVASTSPGIHHAHWVFLRN

Signal sequence: amino acids 1-41

Transmembrane domain: amino acids 325-344

N-glycosylation site: amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site: amino acids 8-12,
 146-150, 252-256, 270-274, 313-317, 362-366, 364-368, 380-384,
 467-471, 468-472

N-myristoylation site: amino acids 4-10, 61-67, 169-175,
 203-209, 387-393, 418-424, 478-484

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 394-405

APPROVED	G. FIG.	
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FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCGGTGGCCTAGAGA
 TGCTGCTGCCGCGGTTGCAGTTGTCGCGCACGCCTCTGCCCGCCAGCCCGCTCCACCGCCGT
 AGCGCCCGAGTGTGCGGGGGGCGCACCCGAGTTCGGGCCATGAGGCCGGGAACCGCGCTACAGG
 CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCCTGCTGAGTGCC
 TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTA
 TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT
 GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA
 AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
 GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT
 CACAATTTAGGAACTGGTATGTGGATGAGCCGTCCTGCGGCAGCGAGGTCTGCGTGGTTCATG
 TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCCCTACATGTTCCAGTGGAATGATGA
 CCGGTGCAACATGAAGAACAATTTCAATTTGCAATATTCTGATGAGAAACCAGCAGTTCCTT
 CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
 GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
 CCTAATCCCCAGCATTCCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTT
 GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC
 TGGCCCTCTCCTCACCAGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
 AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCAATTCAGAGTGTGTT
 CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
 GAAAGTGGGTTTGTGACTCTGGTGAGCGTGAGAGTGGATTTGTGACCAATGACATTTATGA
 GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG
 GTTATTAGGACATATAAAAACTGAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC
 CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT
 GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTGGCTGTATCCTTTAT
 CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCCAGGTCTGGCACATAGTA
 GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG
 GCAGTGATAAAGATGGGCTGTGGAGCTTGAAAACACCTCTGTTTTCTTCTCTATACAG
 CAGCACATATTATCATAACAGACAGAAAATCCAGAATCTTTTCAAAGCCCACATATGGTAGCA
 CAGGTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTCAAAGAATAAAATCAAATAA
 AGAGCAGGAAAAAAAAA

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FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGTQRPCYKVIYFHDTSRRL
 NFEEAKEACRRDGGQLVSI ESEDEQK LIEKF IENLLPSDGD F WIGLR RREEKQSNSTACQDL
 YAWTDGSI SQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
 SDEKPAVPSREAEGETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPLLLLLLV
 VTTVVCWVWICRKRKREQDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
 KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKES
 GWVENEIYGY

Signal sequence: amino acids 1-21

Transmembrane domain: amino acids 235-254

N-glycosylation site: amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 amino acids 296-300

Casein kinase II phosphorylation site: amino acids 28-32,
 30-34, 83-87, 100-104, 214-218, 222-226, 299-303, 306-310,
 323-327

N-myristoylation site: amino acids 18-24, 37-43, 76-82,
 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
 ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
 GTTTGCCTCCTGCAGCCTCAACCCGAGGGGAGCGAGGGCCTACCACCAATGATCACTGGTGT
 GTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
 AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTTCGACCGCAGC
 CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC
 GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAATC
 AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
 CAATACCATGAGACCACCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT
 GCAGCAAATGTTTGCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
 TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTTCGGAATCTG
 GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAGGACCCATCATCAT
 CCACACTGATGAAGCAGATTGAGAAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGA
 GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTG
 AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
 GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTG
 CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCCAAGGAAGACAGG
 GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
 CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGGCTCATGATG
 TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCT
 GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
 TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT
 TCTTGAATGCCATGTCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
 ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT
 TTAAAATAAAGTGCCTTTATACAATG

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FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMOVVFRHGAR
 SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
 TKVGMQOMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
 GPIIIHTDEADSEVLYPNYQSCWSLRQRTGRRRQTASLQPGISEDLLKKVKDRMGIDSSDKVD
 FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHILES
 NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
 FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

Signal sequence: amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 amino acids 218-222

Casein kinase II phosphorylation site: amino acids 87-91,
 104-108, 320-324

Tyrosine kinase phosphorylation site: amino acids 280-288

N-myristoylation site: amino acids 15-21, 117-123, 118-124,
 179-185, 240-246, 387-393

Amidation site: amino acids 216-220

Leucine zipper pattern: amino acids 10-32

Histidine acid phosphatases phosphohistidine signature: amino
 acids 50-65

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FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
 TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCAATGGCTCTGCTATTCTCCTTGATCCTT
 GCCATTTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGCGGGCTGGTGGGGGGCCT
 CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
 ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
 GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAGGTCCTCATCCA
 ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
 ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA
 GTCCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA
 GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGGCCGCAAAGGTGG
 TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
 TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTTCA
 GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCTG
 AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
 GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACTGGGGAGAAAAGGAGGA
 CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
 AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTTCGTTGCTCAGGGGAGGAG
 CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA
 TGTGGCTGTCATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
 GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
 TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG
 ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACATACATCA
 CCACCTTTCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT
 CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
 CACCATTTGTCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
 TTCTAGAGGAACGGAATTTTAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG
 GCTCTATAATCTAATTAGATATAAAATTTCTGGTAACTTTATTTACAATAATAAAGATAGCAC
 TATGTGTTCAAA

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FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPEAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSVPPEGVRLADGPGHCKGRVEVKHQNQWYTVCTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSSGRLEVLHKGWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence: amino acids 1-15

Casein kinase II phosphorylation site: amino acids 47-51,
97-101, 115-119, 209-213, 214-218, 234-238, 267-271, 294-298,
316-320, 336-340

N-myristoylation site: amino acids 29-35, 43-49, 66-72,
68-74, 72-78, 98-104, 137-143, 180-186, 263-269, 286-292

Amidation site: amino acids 196-200

Speract receptor repeated domain signature: amino acids
29-67, 249-287

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FIGURE 55

ACTGCACTCGGTCTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCCTGCTGTTCTGGCTGCCTGGG
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGGTTCATGGAGACAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATGGTTA
C

APPROV.	D.O. FIG.	
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FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
 KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL
 VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQGKMSI
 PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
 AQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence: amino acids 1-21

Transmembrane domain: amino acids 104-120, 278-292

N-glycosylation site: amino acids 228-232

Glycosaminoglycan attachment site: amino acids 47-51

Casein kinase II phosphorylation site: amino acids 135-139,
 139-143, 253-257

Tyrosine kinase phosphorylation site: amino acids 145-153,
 146-153

N-myristoylation site: amino acids 44-50, 105-111, 238-244,
 242-248, 291-297

Amidation site: amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 6-17

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FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
 AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAATTTCTTCTGGACATCCTC
 CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAA
 GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA
 GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
 CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT
 GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
 GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
 CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA
 GGCATTTCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
 CTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA
 TTTTATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
 TCTGTGTCCTAATTTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
 CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
 ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCTGAGCGTTT
 CCTGGCAGTTTTTAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
 AAGCGCAATTAAGCACCTAGTTTTCTGAAAACCTGATTTACCAGGTTTAGGTTGATGTCATCTA
 ATAGTGCCAGAATTTTAATGTTTGAACCTTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA
 TCATTTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT
 ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
 CCAAATGACTTTATTAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
 AATTTGTACCATAACCGTTTATTTAACATATATTTTATTTTTGATTGCACTTAAATTTTGT
 ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
 TGAAGGACTATATCTAGTGGTATTTTACAATGAATATCATGAACTCTCAATGGGTAGGTTTC
 ATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
 GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG
 GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
 AA
 AA

APPROVED	S.D. FIG.	
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FIGURE 58

MKFLLDIILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKPNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

Signal sequence: amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 30-34, 283-287

Casein kinase II phosphorylation site: amino acids 52-56,
95-99, 198-202, 267-271

N-myristoylation site: amino acids 43-49, 72-78, 122-128,
210-216

FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTC
 AGGGAGGAGCACCGACTGCGCCGCACCCTGAGAGATGTTGGTGCCATGTGGAAGGTGATTG
 TTTTCGCTGGTCCTGTTGATGCCTGGCCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
 GTTTCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC
 TGGGAAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCCAGGACTGAACATGA
 AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTC
 TTTCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG
 AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTACAAGTAACATGA
 CCTTGCGTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCA
 GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
 AGCACGGGATTTATACAGTGCACCTAATTCAGTTTTTCCAGATATTTCTGAATATAAAAAATA
 ATGACTTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
 ATCCATTCCCTCAACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
 TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCT
 TGTGGATGAGAAGCAAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
 AGGAAGCAGAACTGGTTTGGAGGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC
 AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT
 GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTTGTCACTCCCAGAGGTGAGACAA
 GCCATCCACGTGGGGAATCAGACTTTTAAATGATGGAACCTATAGTTGAAAAGTACTTGCGAGA
 AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
 TCTACAATGGCCAACCTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC
 ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTTGGAAGATCTTTAA
 ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC
 GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
 TTCATTTATGGAAGGATGGGATCCTTATGTTGGATTAAACTACCTTCCCAAAGAGAACAT
 CAGAGGTTTTTATGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAA
 TTATCTTTTCATATCTGCAAGATTTTTTTTCATCAATAAAAATTATCCTTGAAACAAGTGAGC
 TTTTGTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA
 TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
 AATTTTAGGGTCTTGAATAGGAAGTTTTAATTTCTTCTAAGAGTAAGTGAAGGTGCAGTTG
 TAACAAACAAAGCTGTAACATCTTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
 GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCCAAATAAATGGATGAAGCTATAA
 TAGTTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAAT
 AAAATATTATATATAAAAGTAAAAA

APPROVED	R.G. FIG.	
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FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGD SGQPLFLTPYIEAGKIQKGRELSL
 VGPFPG LNMKSYAGFLTVNKTYN SNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFEH
 GPYVVT SNMTLRDRDFPWT T T L S M L Y I D N P V G T G F S F T D D T H G Y A V N E D D V A R D L Y S A L I Q F
 FQIFPEYKNND FYVTGESYAGKYVPAIAH L I H S L N P V R E V K I N L N G I A I G D G Y S D R E S I G G
 YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGD L T S D P S Y F Q N V T G
 CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
 EIMNNYKVLIYNGQLDIIVAAALTE R S L M G M D W K G S Q E Y K K A E K K V W K I F K S D S E V A G Y I R Q
 AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence: amino acids 1-22

N-glycosylation site: amino acids 81-85, 132-136, 307-311,
 346-350

Casein kinase II phosphorylation site: amino acids 134-138,
 160-164, 240-244, 321-325, 334-338, 348-352, 353-357, 424-428

Tyrosine kinase phosphorylation site: amino acids 423-432

N-myristoylation site: amino acids 22-28, 110-116, 156-162,
 232-238

Serine carboxypeptidases, serine active site: amino acids
 200-208

Crystallins beta and gamma 'Greek key' motif signature: amino
 acids 375-391

FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACAT
 TTTTCCCTTTTCTAACAAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTCTTCTT
 GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG
 CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
 TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
 CTGGGGGAGGGCCTGCCTAACAAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
 AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATTGACTGGCTGGG
 TGAACCTAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
 TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
 GACCAAAATAGATAACAGGATTCCCTGAACATTCTAAGAGGGAGAAAGTATGTTAAAAATA
 GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCCTGGGTC
 AGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTTGGTCTGACCACTCTGCCTTGTGTTTT
 GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
 CCTACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
 ACAGCCGCTCTGTGGTCCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCCCAGCAGCCGGC
 ATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT
 CCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
 ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
 CCCCTCATCGTGAGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAGCTGCT
 CATCATTGACTACTCTGAGAACCGCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCA
 AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
 CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA
 TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCCA
 GCCGGAAGCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
 TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACAT
 CTTCTACATCTACGGCTTTGCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA
 CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGG
 CTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGC
 CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC
 AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAG
 CAGTATCACCAACCGCCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGGCCATCAACTT
 GCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC
 TGCTGGGGAAGGACGTCCAGTGACGAAGGCGCCTGTCCCATCGATGATAACTTCTGTGGA
 CTGGACATCAACCAGCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCAC
 CAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTG
 TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC
 ATTCACCTCCTCAGCAAAGAGTCCCTCTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAG
 GCAACTTTATTTTCTTGGGGAACAAAGGTGAATGGGGAGGTAAGAAGGGGTAAATTTTGTG
 ACTTAGCTTCTAGCTACTTCCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
 TTTCAATATTTCCCAAACCTTAAGAAAAAAGCTTTAAGAAGGTACATCTGCAAAAGCAAA

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FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
 RALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
 YKLTGNLTIQVAHKTGPEEDNKSRYPPPLIVQPCSEVLTLTNVVKLLIIDYSENRLACGSL
 YQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
 FPTLSSRKLPDPRESSAMLDYELHSDVFVSSLIKIPSDTLALVSHFDIFYIYGFASSGGFVYFL
 TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAAYLAKP
 GDSLAQAFNITSQDDVLF AIFSKGQKQYHHPDDSALCAFPPIRAINLQIKERLQSCYQEGN
 LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
 YSVVFVGTKSGKLKKVRVYEFRCSSNAIHLLSKESLLEGSYWWRFNRYQLYFLGEQR

Signal sequence: amino acids 1-32

Transmembrane domain: amino acids 71-87

N-glycosylation site: amino acids 130-134, 145-149, 217-221,
 381-385

Casein kinase II phosphorylation site: amino acids 139-143,
 229-233, 240-244, 291-295, 324-328, 383-387, 384-388, 471-475,
 481-485, 530-534

N-myristoylation site: amino acids 220-226, 319-325, 353-359,
 460-466, 503-509

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FIGURE 63A

AGGCTCCCGCGCGCGGCTGAGTGCGGACTGGAGTGGGAACCCGGGTCCCGCGCTTAGAGAA
CACGCGATGACCACGTGGAGCCTCCGGCGGAGGCCGGCCCGCACGCTGGGACTCCTGCTGCT
GGTCGTCTTGGGCTTCCTGGTGCTCCGCAGGCTGGACTGGAGCACCTGGTCCCTCTGCGGC
TCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGAACCTCATGCTGGAGGATTCCACC
TTCTGGATCTTCGGGGGCTCCATCCACTATTTCCGTGTGCCCAGGGAGTACTGGAGGGACCG
CCTGCTGAAGATGAAGGCCTGTGGCTTGAACACCCTCACCACCTATGTTCCGTGGAACCTGC
ATGAGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCTTCGTCTG
ATGGCCGCAGAGATCGGGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGCAGTGAGAT
GGACCTCGGGGGCTTGCCCAGCTGGCTACTCCAAGACCCTGGCATGAGGCTGAGGACAACTT
ACAAGGGCTTCACCGAAGCAGTGGACCTTTATTTTGACCACCTGATGTCCAGGGTGGTGCCA
CTCCAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATGGTTCCTA
TAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGG
AACTGCTCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTG
GCCACCATCAACTTGCAGTCAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGT
CCAGGGGACTCAGCCCAAGATGGTGATGGAGTACTGGACGGGGTGGTTTGACTCGTGGGGAG
GCCCTCACAATATCTTGGATTCTTCTGAGGTTTTGAAAACCGTGTCTGCCATTGTGGACGCC
GGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATGGAGC
CATGCACTTCCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGCTGACAG
AAGCCGGCGATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGC
ATCCCTCTCCCTCCCCACCTGACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGT
CTTGTAACCTGTCTCTGTGGGACGCCCTCAAGTACCTGGGGGAGCCAATCAAGTCTGAAAAGC
CCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCCTTCGGGTACATTCTC
TATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGGT
GTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCC
TGATCCAGGGTTACACCGTGCTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGG
GAGAATATTGATGACCAGCGCAAAGGCTTAATTGGAAATCTCTATCTGAATGATTACCCCT
GAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGAGCTTCTTTCAGAGGTTTCGGCCTGG
ACAAATGGNGTTCCCTCCCAGAAACACCCACATTACCTGCTTTCTTCTTGGGTAGCTTGTCC
ATCAGCTCCACGCCTTGTGACACCTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTGTATT
CATCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCCAGAAGACGCTTTACCTCC

_____ To Figure 63B

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FIGURE 63B

From 63A

CAGGTCCCTGGTTGAGCAGCGGAATCAACCAGGTCATCGTTTTTGGAGGAGACGATGGCGGGC
CCTGCATTACAGTTACACGAAACCCCCACCTGGGCAGGAACAGTACATTAAGTGAGCGGT
GGCACCCCCTCCTGCTGGTGCCAGTGGGAGACTGCCGCCTCCTCTTGACCTGAAGCCTGGTG
GCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGGACTGGGGG
CTACAGTCTGCCCCTGTCTCAGCTCAAAACCCTAAGCCTGCAGGGAAAGGTGGGATGGCTCT
GGGCCTGGCTTTGTTGATGATGGCTTTCCTACAGCCCTGCTCTTGTCGCGAGGCTGTCGGGC
TGTCTCTAGGGTGGGAGCAGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGCTG
AAACGTGCCCTTGCACCGGACGTACAGCCCTGCGAGCATCTGCTGGACTCAGGCGTGCTCT
TTGCTGGTTCCCTGGGAGGCTTGGCCACATCCCTCATGGCCCCATTTTATCCCCGAAATCCTG
GGTGTGTCACCAGTGTAGAGGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTTCTTCC
TTCACAACCTTCTGAGCCTTCTTTGGGATTCTGGAAGGAACTCGGCGTGAGAAACATGTGAC
TTCCCCTTTCCCTTCCCCTCGCTGCTTCCCACAGGGTGACAGGCTGGGCTGGAGAAACAGA
AATCCTCACCTGCGTCTTCCAAGTTAGCAGGTGTCTCTGGTGTTCACTGAGGAGGACATG
TGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGGACAGAAGGCCAG
CTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGGACAGA
AGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGG
AGGACAGAAGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATC
CAGGGAGGAGGACAGAAGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCACGCCGAACA
GCAGGGGACAGCAGCCCTCCTTCGAAGTGTGTCCAAGTCCGCATTTGAGCCTTGTTCTGGG
GCCAGCCCAACACCTGGCTTGGGCTCACTGTCCTGAGTTGCAGTAAAGCTATAACCTTGAA
TCACAA

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FIGURE 64

MTTWSLRRRPARTLGLLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW
 IFGGSIHYFRVPREYWRDRLLKMKACGLNTLT TYVPWNLHEPERGKFD FSGNLDLEAFVLMA
 AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDHLMSRVVPLQ
 YKRGGP I IAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKDGLSKGIVQGVLAT
 INLQSTHELQLLTTFLFNVQGTQPKMVM EYWTGWFD SWGGPHNILDSSEVLKTYSAIVDAGS
 SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDY TAKYMKLRDEFGSISGIP
 LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYILYE
 TSITSSGILSGHVHDRGQVFVNTV SIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN
 IDDQRKGLIGNLYLND SPLKNFRIYSLDMKKSFFQRFG LDKWXSLPETPTLP AFFLGSLSIS
 STPCDTFLKLEGWEKG VVFINGQNLGRYWNIGPQKTLYLP GPWLSSGINQVIVFEETMAGPA
 LQFTETPHLGRNQYIK

Signal sequence: amino acids 1-27

Casein kinase II phosphorylation site: amino acids 141-118,
 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site: amino acids 146-152, 236-242, 240-246,
 244-250, 287-293, 309-315, 320-326, 366-372, 423-429, 425-431,
 441-447, 503-509, 580-586

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FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
 CTGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG
 GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
 CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
 AAGAAGCTGTCCTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
 GGCAGACACTCGGTTCGTTTCGTAGTGGATAGGGGTCATGACCGGTTTCTCCTAGACGGGGCCC
 CGTTCGCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCCGAC
 CGGCTTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTTATGTGCCCTGGAACATA
 CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTTGCCCTTTCTGA
 ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG
 TGGGAGATGGGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC
 AGATCCAGACTTCCTTGCCGCAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC
 CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTTCAGGTGGAGAATGAATATGGTAGC
 TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGGCTCTTCCGTGCACTGCTAGG
 AGAAAAGATCTTGCTCTTCACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
 GACTCTATAACCACTGTAGATTTTGGCCCAGCTGACAACATGACCAAATCTTTACCCTGCTT
 CGGAAGTATGAACCCCATGGGCCATTGGTAACTCTGAGTACTACACAGGCTGGCTGGATTA
 CTGGGGCCAGAATCACTCCACACGGTCTGTGTGAGCTGTAACCAAAGGACTAGAGAACATGC
 TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG
 AATGGTGCCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC
 TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTTGCTCTTCGAGATGTCATCAGCAAGT
 TCCAGGAAGTTCCCTTGGGACCTTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
 ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCCCAT
 TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC
 GAACCTATATGACCCATACCATTTTTTGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTC
 CATGACCGTGCTATGTGATGGTGGATGGGGTGTTCAGGGTGTGTGGAGCGAAATATGAG
 AGACAAACTATTTTTGACGGGGAACTGGGGTCCAACTGGATATCTTGGTGGAGAACATGG
 GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG
 GGGCAAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
 GTGGTTTTCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT
 ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
 ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGGCCGGTACTGGACAAAGCAGGGGCC
 ACAACAGACCCTCTACGTGCCAAGATTCCTGCTGTTTCCTAGGGGAGCCCTCAACAAAATTA
 CATTGCTGGAAGTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTTGGATAAGCCTATC
 CTCAATAGCACTAGTACTTTGCACAGGACACATATCAATTCCTTTTCAGCTGATACACTGAG
 TGCTCTGAACCAATGGAGTTAAGTGGGCACTGAAAGGTAGGCCGGGCATGGTGGCTCATGC
 CTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTGAGGACTTCAAGA
 CCAGCCTGGCCAACATGGTGAAACCCCGTCTCCACTAAAAATACAAAAATTAGCCGGGCGTG
 ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
 AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
 GACACTCCATCTCAAAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRS FVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLA AVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TL LRKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNM YMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLEPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSGDFTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence: amino acids 1-27

N-glycosylation site: amino acids 97-101, 243-247, 276-280,
486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 4-8

Casein kinase II phosphorylation site: amino acids 148-152,
234-238, 327-331, 423-427, 469-473, 550-554, 603-607, 644-648

Tyrosine kinase phosphorylation site: amino acids 191-198

N-myristoylation site: amino acids 131-137, 176-182, 188-194,
203-209, 223-229, 227-233, 231-237, 274-280, 296-300, 307-313,
447-453, 484-490

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FIGURE 67

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
 ACCCACAATATGGCCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
 TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTCAGGATACCTTTGAAGGAATATT
 CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT
 GCGTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT
 CTTGTCAGAAGTTAGTGAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGAGATTG
 AAAAAGCTCAGGCAGCACATTTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
 CTGTCGGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAGT
 AATTCCAGAAGCTAAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC
 TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA
 TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA
 CCTTCGAGAGTTGTACTTAATAGGCAATTTGAAGTCTGAAAACAATAAGATGATAGGACTTG
 AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT
 CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTCATAATGACGGCAC
 TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAAGTCCAGA
 ACTGTGAGCTAGAGAGAATCCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACTGGAT
 TAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAACGACT
 GACTTGTTTTAAATTTATGGCATAACAAAATTGTTACTATTCTCCCTCTATTACCCATGTCA
 AAAACTTGGAGTCACTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT
 AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA
 AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATTCTGC
 CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
 TCACTCCCAGAGAAAGTTGGTCAGCTCTCCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG
 CTTGGACCGCCTGCCAGCCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTTGTTG
 TGGAAGATCACCTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
 AATATTCCTTTTGCAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
 AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
 ATACATCTTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
 GTTCAATGTTTGTAGGGTTTTAAGTCATTCATTTCCAAATCATTTTTTTTTTTCTTTTGGGG
 AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTTCTTTTTTAAATTGTTTGTAAGTGGAT
 GCTGCCGCTACTGAATGTTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
 TTCTTACTAAAAA

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FIGURE 68

MAYMLKKLLISYISIIICVYGFI CLYTLFWLFR IPLKEYSFEK VREESSFSDI PDVKNDFAFL
LHMVDQYDQLYSKRFGVFLSEVSENKLR EISLNHEWTFEKL RQHISR NAQDKQELHLM LSG
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLC HCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLSEN NKMIGLESLREL RHLKILHVKSNTK VPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAE LELQNC ELERIPHAIFSLSNLQELDLKS
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLES LYFSNNKLES LPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSOLTQLELKGNC LDR LPAQLGQCRMLKKSGLVVEDH LFD TLPLEVKEALNQDINIP
FANGI

Signal sequence: amino acids 1-20

N-glycosylation site: amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 326-330

Casein kinase II phosphorylation site: amino acids 48-52,
133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site: amino acids 349-355,
375-381

N-myristoylation site: amino acids 78-84, 124-130, 212-218,
392-398

APPROVED	FIG. 69	
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FIGURE 69

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCCATTCTTTTCATTGACAACTGAC
TTTTTTTATTTCTTTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGA
CATTTGTGTTTTACACACATAAGGATCTGTGTTTGGGGTTTCTTCTTCCCTCCCCTGACATTG
GCATTGCTTAGTGGTTGTGTGGGGAGGGAGACCACGTGGGCTCAGTGCTTGCTTGCACTTAT
CTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTCATCGCTGGTG
GTATCCTGGCGGCCTTGCTCCTGCTGATAGTTGTCTGTCTCTGTCTTTACTTCAAAATACAC
AACGCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAACCCAGACAA
GGTGTGGTGGGCCAAGAACAGCCAGGCCAAAACCATTGCCACGGAGTCTTGTCCTGCCCTGG
AGTGCTGTGAAGGATATAGAATGTGTGCCAGTTTGTATTCCCTGCCACCTTGCTGTTGCGAC
ATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAAAGCAGAGCCCTGAAGACTTCA
ATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAGCTCCCCA
TCAGTTTCATGGAAAATAACTCAGTGCCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAG
AGCTTCCACTGGGGGCAACCCCTCCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGG
AATGCTGATAAACCAGTCACACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCT
GGAAC TGACGTTTCCCTGGAGGTGTCCAGAAAGCTGATGTAACACAGAGCCTATAAAAGCTG
TCGGTCTTAAGGCTGCCCAGCGCCTTGCCAAAATGGAGCTTGTAAGAAGGCTCATGCCATT
GACCTCTTAATTCTCTCCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAATGCAA
GCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAA
CTCAATCCCAGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAAACAAAGCATCAGAAT
TATCTTTTCTATGTCCAGCTTGATCCAGATGGAAGCTGTGAAAGTGAAAACATTAAAGTCT
TTGACGGAACCTCCAGCAATGGGCCTCTGCTAGGGCAAGTCTGCAGTAAAAACGACTATGTT
CCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACTGACTCAGCAAGAAT
TCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCCTAACATCTCTATTCCAAACTGTG
GCGGTTACCTGGATACCTTGGAAGGATCCTTCACCAGCCCCAATTACCCAAAGCCGCATCCT
GAGCTGGCTTATTGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAACTAAACTT
CAAAGAGATTTTCTAGAAATAGACAAACAGTGCAAATTTGATTTTCTTGCCATCTATGATG
GCCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGTGGCCGTGTGACTCCCACCTTCGAA
TCGTTCATCAAACCTCTCTGACTGTCTGTGTTGTCTACAGATTATGCCAATTCTTACCGGGGATT
TTCTGCTTCTTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTT
CTGACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAAT
AACTTGCAACTAAAAGACCCAACCTTGACAGACCAAAATTATCAAATGTTGTGGAATTTTCTGT
CCCTCTTAATGGATGTGGTACAATCAGAAAGGTAGAAGATCAGTCAATTACTTACACCAATA
TAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACCCGTCAGAAACAACTCCAGATT
ATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACAGAAGATGA
TGTAATACAAAGTCAAAATGCACTGGGCAAATATAACACCAGCATGGCTCTTTTGAATCCA
ATTCATTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTTGAACCAAACTCTTTT
GTTCAAGTTAGTCTGCACACCTCAGATCCAAATTTGGTGGTGTCTTCTTGATACCTGTAGAGC
CTCTCCCACCTCTGACTTTGCATCTCCAACCTACGACCTAATCAAGAGTGGATGTAGTCGAG
ATGAAACTTGTAAGGTGTATCCCTTATTTGGACACTATGGGAGATTCCAGTTTAATGCCTTT
AAATTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAGTTTTTGATATGTGATAGCAG
TGACCACAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCAT
ATAAATGGAAAACAGATTCCATCATAGGACCCATTCGTCTGAAAAGGGATCGAAGTGCAAGT
GGCAATT CAGGATTT CAGCATGAAACACATGCGGAAGAACTCCAAACCAGCCTTTCAACAG
TGTGCATCTGTTTTCTTCATGGTTCTAGCTCTGAATGTGGT GACTGTAGCGACAATCACAG
TGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTGCAGA ACTAT TAACTA
ACAGGTCCAACCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGTGG
CTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAA
AAA

APPROVED	FIG.	
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FIGURE 70

MELVRRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
 ERPENKSIRIIFSIVQLDPDGSCSENIKVFDGTSSNGPLLQGVCCKNDYVPVFESSSSTLT
 FQIVTDSARIQRTVFVFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
 EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVLS
 TDYANSYRGFSASYTSIYAENINTTSLTSSDRMRVVISKSYLEAFNSNGNNLQLKDPTCRP
 KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQQLQIIVKCEMGNST
 VEIIYITEDDVIQSQUALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
 LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
 QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFQHETHA
 EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence: amino acids 1-24

Transmembrane domain: amino acids 571-586

N-glycosylation site: amino acids 29-33, 57-61, 67-71,
 148-152, 271-275, 370-374, 394-398, 419-423

Casein kinase II phosphorylation site: amino acids 22-26,
 108-112, 289-293, 348-352, 371-375, 379-383, 408-412, 463-467,
 520-524, 556-560

Tyrosine kinase phosphorylation site: amino acids 172-180,
 407-415, 407-416, 519-528

N-myristoylation site: amino acids 28-34, 38-44, 83-89,
 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGAC**ATG**CGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGC
TGCTGCCGCCGCCGCCGTGCCCTGCCACAGCGCCACGCGCTTCGACCCACCTGGGAGTCC
CTGGACGCCCCGCCAGCTGCCCGCGTGGTTTTGACCAGGCCAAGTTCGGCATCTTGATCCACTG
GGGAGTGTTTTCCGTGCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAAGGAAA
AGATAACCGAAGTATGTGGAATTTATGAAAGATAATTACCTCCTAGTTTCAAATATGAAGAT
TTTGGAACCACTATTTACAGCAAAATTTTTTAATGCCAACCAGTGGGCAGATATTTTTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT
CAGAATATTCGTGGAACCTGGAATGCCATAGATGAGGGGGCCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTTTGACTGTACTATTCCCTTTTTTGA
ATGGTTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGCCCTGGTT
ATATAATGAAAGCCCAGTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAAACCTGCATGACAATAGACAACTGTCCTGGGGCTATAGGAGGGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTCATGTG
GAGGAAATCTTTTGATGAATATTGGGCCCACACTAGATGGCACCATTTCTGTAGTTTTTGAG
GAGCGACTGAGGCAAGTGGGGTCTTGCTAAAGTCAATGGAGAAGCTATTTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTTCCCTTGCCAT
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAACTACTGGGCCATGGACAGCCACTTAACTG
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTTCATCAGATGC
CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATC**TAA**AGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACTGGATAAGAAAATTATTTGGCAGTTCAGCCCTTTCCCTTTTTTCCCACTA
AATTTTTCTTAAATTACCCATGTAACCATTTTAACTCTCCAGTGCACCTTTGCCATTAAAGTC
TCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAAT
TTTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAACATAGAGAA
GTACAGTAAAAATACTGTAAAATAAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAA
GTTTTTCTTTCTTCAATTATAAATTAACATAAGTGTACTGTAACCTTTACAAACGTTTTAATT
TTTAAACCTTTTTGGCTCTTTTGTAATAACACTTAGCTTAAACATAAACTCATTGTGCAA
ATGTAA

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FIGURE 72

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYWQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence: amino acids 1-28

N-glycosylation site: amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site: amino acids 32-36,
182-186, 209-213, 227-231, 276-280, 315-319, 375-375

Tyrosine kinase phosphorylation site: amino acids 361-369,
389-397

N-myristoylation site: amino acids 143-149, 178-184, 255-261,
272-278, 428-434

Leucine zipper pattern: amino acids 410-432

Alpha-L-fucosidase putative active site: amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
 TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
 TGAGGTGTTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
 CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCT
 TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCCTTGTGAGCAAAAAGGCCGAACCAGC
 AGCTGAATTTACAGAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
 GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGA
 TGGATTCTGTGGTTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
 TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT
 ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCA
 AACTGCAACACAAACAACAGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTT
 ACTCTACAATACCTGCCCCCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCACG
 AGAAAAAATTTGATTTGTGTACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAAAC
 TGAACCATTTGTTGAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCC
 CCACGGCTCTGCTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGC
 TATGTCAAAAGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT
 CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGA
 AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAA
 GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTTCTTTCATGCTCC
 TTACCCTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCCTT
 GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC
 CCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC
 TTTCTAGCCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAA
 GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAGGCCTCCTGGCTGTCTGAGGCTAGG
 TGGGTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGAC
 CCTTCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTA
 AGAGCAAAAGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
 ACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT
 GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGA
 ATCACTGTTTGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT
 AGGAAATATACTTTTACAAGTAACAAAAATAAAACTCTTATAAATTTCTATTTTTATCTGA
 GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAGTAATAAAATTCA
 ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
 TGAATATTATTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTTCA
 GTTTTGATATTTCTAGCTTATCTACTTCCAACTAATTTTTTATTTTGCTGAGACTAATCTT
 ATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAACATACCTAAGAAG
 TACATTGTTACCTCTATATACCAAAGCACATTTTAAAAGTGCCATTAACAAATGTATCACTA
 GCCCTCCTTTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA
 AGCATTTAGAAAACCTT

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FIGURE 74

MARCFSLVLLLTSIWTTLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
 LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLWKVPVSRQF
 AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
 APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGGVPTALLVLALLFF
 GAAAGLGFCYVKRYVKAFPFNTKNQOKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
 SKTTVRCLEAEV

Signal sequence: amino acids 1-16

Transmembrane domain: amino acids 235-254

N-glycosylation site: amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site: amino acids 145-149,
214-218

Tyrosine kinase phosphorylation site: amino acids 79-88

N-myristoylation site: amino acids 23-29, 65-71, 234-240,
235-239, 249-255, 253-259

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FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGTATTTCGGTGCCGCGACTTTCACGATGG
 CTCGCCCCAACCTTACTACCTTCTGTGCGGCCCTGCTCTCTGCTGCCTTCCTACTCGTGAGGAA
 ACTGCCGCGGCTCTGCCACGGTCTGCCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTG
 ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
 TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT
 TCTTTTCTTCCGCTTGGATATTCGCATGGGCCTACTTTACATCACACTCTGCATAGTGTTC
 TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
 ACCATTGATGAGGAAC TAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAA
 TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAC
 GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
 AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA
 GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG
 AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAAACTATCA
 AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGA
 TGGGGAAAACAAGAAGGATAAATAAGATCCTCACTTTGGCAGTGCTTCCTCTCCTGTCAATT
 CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGG
 CTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG
 GCACCCTACAGGAAGGCCTGCCATGCTGTGGCCAACTGTTTCACTGGAGCAAGAAAGAGATC
 TCATAGGACGGAGGGGGAAATGGTTTCCCTCCAAGCTTGGGTCAGTGTGTTAACTGCTTATC
 AGCTATTCAGACATCTCCATGGTTTCTCCATGAAACTCTGTGGTTTCATCATTCCTTCTTAG
 TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAA
 CGCTAAGAATTTTCCCCCAAGGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTC
 TTCATTAAAAGTATAAGCCTAACTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAAG
 TTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA
 TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCCTGGACTTTCAC
 TAACCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAAGATTGGGATT
 TCCTTTTG

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FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVKLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPYADLSLKYN
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK.

Signal sequence: amino acids 1-48

Transmembrane domain: amino acids 111-125

N-glycosylation site: amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 154-158, 265-269

Casein kinase II phosphorylation site: amino acids 51-55,
145-149, 245-249, 286-290, 288-292

N-myristoylation site: amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1: amino acids
244-253

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FIGURE 77

[illegible]

APPROVED	25. FIG.	
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FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
 GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDLVAIGLRHRSFGDYQGRVHLRQD
 KEHDVSLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
 VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
 HRRLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR
 CDAGWLADGSVRYPVVHPPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence: amino acids 1-17

Casein kinase II phosphorylation site: amino acids 29-33,
 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site: amino acids 137-145

N-myristoylation site: amino acids 36-42, 184-190, 208-214,
 237-243, 297-303, 307-313

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FIGURE 80

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
 EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
 YDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGD SMATRE
 ELTAFLHP EEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEP AWVQTERQQ
 FRDFRDLNKDGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
 GSQATNYGEDLTRHHDEL

Signal sequence: amino acids 1-20

N-glycosylation site: amino acids 140-144

Casein kinase II phosphorylation site: amino acids 72-76,
 98-102, 127-131, 184-188, 208-212, 289-293, 291-295, 298-302

N-myristoylation site: amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence: amino acids 325-330

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FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
 GCGGCGGGCGCGGGTGCAGGGATCCCTGACGCTCTGTCCCTGTTTCTTTGTCGCTCCCAG
 CCTGTCTGTCTGTCGTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTGCACACCGATCCTG
 GGCTTCGCTCGATTTGCCGCCGAGGCGCCTCCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG
 CGGGTCTGTCTGTGTCCTCTCTCCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGCAGGGGCTCT
 GAGGAGGTGACGCGCGGGGCTCCCGCACCTTGGCCTTGCCCGCATTCTCCCTCTCTCCCAG
 GTGTGAGCAGCCTATCAGTCACCATGTCGCGCAGCCTGGATCCCGGCTCTCGGCCTCGGTGTG
 TGTCTGCTGCTGCTGCCGGGGCCCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG
 TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGGCTGCC
 CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
 GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACC
 TGGTCGAGAAACTATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT
 GGTCTGCTTCTTTACAGTAACTAAAGGCCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
 GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAAGTGG
 CAATAAAGATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC
 GCCGATTTAATTTACAGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA
 GAAGGACCACATGTGGGCCTTGTTCAGCCAGTGAACATCCCAAATAGAAATTTTACTTGAA
 AAATTTTACATCAGCCAAAGATGTTTTGTTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA
 ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATCTTCACGGTAGATGCTGGA
 GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACAT
 CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA
 AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTCACATTTGTTGACAAGGCTGTCTGT
 CGGAATAATGGCTTCTTCTCTTACCACATGCCCAACTGGTTTGGCACCACAAATACGTAAA
 GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT
 CAGTGAACATTGCCTTTCTAATTGATGGCTCCAGCAGTGTTGGAGATAGCAATTTCCGCCCTC
 ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAAATCTCGGACATTGGTGCCAAGAT
 AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTCAGTTTCACTGACTATAGCACCA
 AAGAGAATGTCCTAGCTGTCATCAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT
 GATGCCATTTCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAAGAA
 CTTCTAGTAATTGTCACAGATGGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG
 CACATGATGCAGGAATCACTATCTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG
 AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTCAAGAGAGTTCACAGGATT
 AGAACCAATTGTTTCTGATGTCATCAGAGGCATTGTAGAGATTTCTTAGAATCCCAGCAAT
AATGGTAACATTTTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAAATTGTATT
 CTCATAATACTGAAATGCTTTAGCATACTAGAATCAGATACAAAACCTATTAAGTATGTCAAC
 AGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT
 ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA
 GATAATGTGGATTAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA
 TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAAAA

APPROVED	D.C. FIG.	
BY	CLASS	SUBCLASS
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FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEF SVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAlKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKV VVV FIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVT FVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNI AF LI
DGSSSVGDSNFRLMLEFVSNI AKT FEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAF FTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence: amino acids 1-24

N-glycosylation site: amino acids 100-104, 221-225

Casein kinase II phosphorylation site: amino acids 102-106,
129-133, 224-228, 316-320, 377-381, 420-424, 425-429, 478-482,
528-532

N-myristoylation site: amino acids 10-16, 23-29, 81-87,
135-141, 158-164, 205-211, 239-245, 240-246, 261-267, 403-409,
442-448, 443-449

Amidation site: amino acids 145-149

APPROVED	D.E. FIG.	
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FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCAGCCC
GGCGGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG
GGGCGGCGGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTTGGGGCCACCCTGCTGTGCCTGC
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCGGCCCGGCTCTCAGCTACCCGCAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGA
GGTTGAGGAACTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCAGCTAT
CACAATGAGACCAACACAGACACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCCAGC
ATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAA
TGGCCACCAGGGGCAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGGCTG
TGCTGTGCCTTCCAGAGAGGCCTGCTGTTCCCTGTGTGCACACCCTGCCCGTGGAGGGCGA
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCCGCT
GCACTGCTGGGAGGGGAAGAGATTTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA
ATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCTTACA
TCTTCTTCCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTCAGC
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAAC
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCCTTACCAGTTGGCAG
ACAGCCGTTTGTCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTCTGATTGGTTTTTGGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAA
CCTGGCAAAAATGCAACAAATGAATTTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTG
TGCTTTCAGCTGTTGCAGATGAAATGTTCTGTTTACCCTGCATTACATGTGTTTATTCATCC
AGCAGTGTTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC
CCTCTCTCAGCACAGCCTGGGGAGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCAT
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTTCTTGAGGCATGCACATCTGGAATTAAG
GTCAAATAATTCTCACATCCCTCTAAAGTAACTACTGTTAGGAACAGCAGTGTTCTCAC
AGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT
TGCATTAGTAACTTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTTCATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGATTGTA
TAAGCATGCTTTCTTTGAGTTTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGC
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

APPROVED	H.C. FIG.	
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FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAAKASSEVNLANLPSPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQQRMLCTRDSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPLCCAFQRGLLFPVCTPLPVEGELCHDPA SRL
LDLITWELEPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEI

Signal sequence: amino acids 1-19

N-glycosylation site: amino acids 96-100, 106-110, 121-125,
204-208

Casein kinase II phosphorylation site: amino acids 46-50,
67-71, 98-102, 135-139, 206-210, 312-316, 327-331

N-myristoylation site: amino acids 202-208, 217-223

Amidation site: amino acids 140-144

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FIGURE 85A

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGGCT
CAGAAGGACTCTGAAGATAACAATAATTTTCAGCCCATCCACTCTCCTTCCCTCCCAAACACA
CATGTGCATGTACACACACACATACACACACATACACCTTCCTCTCCTTCACTGAAGACTCA
CAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACACTAAAGCCTTAAGGACAGGCCTGG
CCATTACCTCTGCAGCTCCTTTGGCTTGTTGAGTCAAAAAACATGGGAGGGGGCCAGGCACGG
TGA CTCACACCTGTAATCCCAGCATTTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTCAG
GAGTTCGAGACCAGCCTGGCCAACATGGAGAAACCCCATCTCTACTAAAAATACAAAAATT
AGCCAGGAGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAATC
GCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCGCTGCACTCCAGCCTGGGT
GACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGAGGGGTAGATACTGCTTCTCT
GCAACCTCCTTAACTCTGCATCCTCTTCTTCCAGGGCTGCCCCCTGATGGGGCCTGGCAATGA
CTGAGCAGGCCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGA
CGCCCGGTGTAGAATGACTGCCCTGGGAGGGTGTTTCTTGGGCCCTGGCAGGGTTGCTGAC
CCTTACCCTGCAAAACACAAAGAGCAGGACTCCAGACTCTCCTTGTGAATGGTCCCCTGCCC
TGCAGCTCCACCATGAGGCTTCTCGTGGCCCCACTCTTGCTAGCTTGGGTGGCTGGTGCCAC
TGCCACTGTGCCCCGTGGTACCCTGGCATGTTCCCTGCCCCCCTCAGTGTGCCTGCCAGATCC
GGCCCTGGTATACGCCCCGCTCGTCTTACCGCGAGGCTACCACTGTGGACTGCAATGACCTA
TTCTTGACGGCAGTCCCCCGGCACTCCCCGCAGGCACACAGACCCTGCTCCTGCAGAGCAA
CAGCATTGTCCGTGTGGACCAGAGTGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACC
TGTTCCAGAACAGCTTTTTCGGATGCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTG
AGCCTGCACCTAGAGGAGAACCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGC
CAGCCTACAGGA ACTCTATCTCAACCACAACCAGCTCTACCGCATCGCCCCAGGGCCTTTT
CTGGCCTCAGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGC
CGCTGGTTTGAAATGCTGCCCAACTTGAGATACTCATGATTGGCGGCAACAAGGTAGATGC
CATCCTGGACATGAACTTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGA
ACCTGCGGGAGATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTC
TATGACAACCAGCTGGCCCCGGGTGCCAGGCGGGCACTGGAACAGGTGCCCGGGCTCAAGTT
CCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGCCAACATGCTGC
ACCTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTG
GTGAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCCTTCATCCA
CCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCTCATGCTCAACAACAACGCTCTCA

To Figure 85B

APPROVED	FIG.	
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FIGURE 85B

From Figure 85A

GTGCCTTGCACCAGCAGACGGTGGAGTCCCTGCCAACCTGCAGGAGGTAGGTCTCCACGGC
AACCCCATCCGCTGTGACTGTGTTCATCCGCTGGGCCAATGCCACGGGCACCCGTGTCCGCTT
CATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCCGGTCCGTG
AGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGCCCTCATCTCCCCACGAAGCTTCCCC
CCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGCACTGGCCGAACC
CGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGACTGACACCTGCCCATGCAGGCA
GGAGGTACCGGGTGTACCCCGAGGGGACCCCTGGAGCTGCGGAGGGTGACAGCAGAAGAGGCA
GGGCTATACACCTGTGTGGCCAGAACCTGGTGGGGGCTGACACTAAGACGGTTAGTGTGGT
TGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACAGGGGCTGGAGCTCCGGGTGC
AGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTCACCCACCCAACACAGTGTCCACC
AACCTCACCTGGTCCAGTGCCCTCCTCCCTCCGGGGCCAGGGGGCCACAGCTCTGGCCCGCCT
GCCTCGGGGAACCCACAGCTACAACATTACCCGCCTCCTTCAGGCCACGGAGTACTGGGCCT
GCCTGCAAGTGGCCTTTGCTGATGCCCACACCCAGTTGGCTTGTGTATGGGCCAGGACCAA
GAGGCCACTTCTTGCCACAGAGCCTTAGGGGATCGTCCTGGGCTCATTGCCATCCTGGCTCT
CGCTGTCCTTCTCCTGGCAGCTGGGCTAGCGGCCACCTTGGCACAGGCCAACCCAGGAAGG
GTGTGGGTGGGAGGCGGCCTCTCCCTCCAGCCTGGGCTTCTTGGGGCTGGAGTGCCCTTCT
GTCCGGGTTGTGTCTGCTCCCCCTCGTCCTGCCCTGGAATCCAGGGAGGAAGCTGCCCAGATC
CTCAGAAGGGGAGACACTGTTGCCACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTC
AGCAGTAGAGAAATCACTAGGACTACTTTTTACCAAAGAGAAGCAGTCTGGGCCAGATGCC
CTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGCCTGGCAGCTGGGCCAAGACAGATGG
GGCTTTGTGGCCCTGGGGGTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTC
ACCTCTGCTGCCATTCTGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCC
TGCTCCCCATCTTCTCTCTGCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCCTACCTGT
GTCCCCGGGCTGCACCCCTTCCTCTTCTCTTTCTCTGTACAGTCTCAGTTGCTTGCTCTTGT
GCCTCCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGCTGCCCTCAATGT
GGGAGTGACCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAACGCCTCATC
TCAGCAGCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGG
AGAAATGTGTCACCTCCCCCAACCCGATTCACTCTTTTCTCCTGTTTTGTAAAAAATAAAAA
TAAATAATAACAATAAAAAAA

APPROVED	FIG. FIG.	
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FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNO
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIKFAVNLP
ELTKLDITNNPRLSFIHPRAFHHLPMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAEEAGLYT
CVAQNLVGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPHYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVGGRRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSSEGETLLPPLSQNS

Signal sequence: amino acids 1-18

Transmembrane domain: amino acids 629-648

N-glycosylation site: amino acids 94-98, 381-385, 555-559,
583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 485-489

Casein kinase II phosphorylation site: amino acids 46-50,
51-55, 96-100, 104-108, 130-134, 142-146, 243-247, 313-317,
488-492, 700-704

Tyrosine kinase phosphorylation site: amino acids 532-540

N-myristoylation site: amino acids 15-21, 493-499, 566-572

Amidation site: amino acids 470-474, 660-664, 692-696

APPROVED	D.C. FIG.	
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FIGURE 87A

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGACA
 TTGTGTACCGCCTCTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATC
 TGCTACACCGTCTACTACGTGCACAACATCAAGTTCGACGTGGACTGCACCGTGGACATTGA
 GAGCCTGACGGGCTACCGCACCTACCGCTGTGCCCACCCCTGGCCACACTCTTCAAGATCC
 TGGCGTCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTACACACTGTGG
 TGGATGCTACGGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTA
 CAGCGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACG
 ACCCGCTCTACTCCAAGCGCTTCGCCGTCTTCCTGTCGGAGGTGAGTGAGAACAAGCTGCGG
 CAGCTGAACCTCAACAACGAGTGGACGCTGGACAAGCTCCGGCAGCGGCTCACCAAGAACGC
 GCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCATCCCTGACACTGTGTTTGACC
 TGGTGGAGCTGGAGGTCCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCGCCAGCATT
 GCCCAGCTCACGGGCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGCGCC
 TCGCTGGCCTTCCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGG
 AGATCCCGCTGTGGATCTATAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTG
 AGCGCGGAGAACAACCGCTACATCGTCATCGACGGGCTGCGGGAGCTCAAACGCCTCAAGGT
 GCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCACAGATGTGGGCGTGCACC
 TGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCCTAACAGCCTCAAGAAG
 ATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCAT
 CTTACGCCCTCCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGG
 AGATCATCAGCTTCCAGCACCTGCACCGCCTCACCTGCCTTAAGCTGTGGTACAACCACATC
 GCCTACATCCCCATCCAGATCGGCAACCTCACCAACCTGGAGCGCCTCTACCTGAACCGCAA
 CAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCGCTACCTGGACCTCA
 GCCACAACAACCTGACCTTCCTCCCTGCCGACATCGGCCTCCTGCAGAACCTCCAGAACCTA
 GCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCG
 GGCCCTGCACCTGGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGGTGGGCGAGCTGACCA
 ACCTGACGCAGATCGAGCTGCGGGGCAACCGGCTGGAGTGCCTGCCTGTGGAGCTGGGCGAG
 TGCCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGAGGACCTGTTCAACACACTGCCACC
 CGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCTGAGCGAGGCCGGCCCAGC
 ACAGCAAGCAGCAGGACCGCTGCCAGTCCTCAGGCCCGGAGGGGCAGGCCTAGCTTCTCCC
 AGAACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCAGGAGCCTGGGGCCGCTTGTGAGT
 CAGGCCAGAGCGAGAGGACAGTATCTGTGGGGCTGGCCCCTTTTCTCCCTCTGAGACTCAGC

_____ To Figure 87B

APPROVED	FIG. 87B	
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FIGURE 87B

From Figure 87A

TCCCCCAGGGCAAGTGCTTGTGGAGGAGAGCAAGTCTCAAGAGCGCAGTATTTGGATAATCA
GGGTCTCCTCCCTGGAGGCCAGCTCTGCCCCAGGGGCTGAGCTGCCACCAGAGGTCCTGGGA
CCCTCACTTTAGTTCTTGGTATTTATTTTTCTCCATCTCCACCTCCTTCATCCAGATAACT
TATACATTCCCAAGAAAGTTTCCAGCCAGATGGAAGGTGTTTCCAGGGAAAGGTGGGCTGCCTTT
TCCCCTTGTCTTATTTAGCGATGCCGCCGGGCATTTAACACCCACCTGGACTTGAGCAGAG
TGGTCCGGGGCGAACCAGCCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTG
CGGTCCACGGGAGAGCAGGCCTCCAGCTGGAAAGGCCAGGCCTGGAGCTTGCTCTTCAGTT
TTTGTGGCAGTTTTAGTTTTTTGTTTTTTTTTTTTTAATCAAAAAACAATTTTTTTTAAAA
AAAAGCTTTGAÂAATGGATGGTTTGGGTATTAAAAAGAAAAAAAAAACTTAAAAAAAAAAAG
ACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAAGCAG
CCAGACGTTGAACTGTGTTTCCCTTCCCTGGGCGCAGGGTGCAGGGTGTCTTCCGGATCTGG
TGTGACCTTGGTCCAGGAGTTCTATTTGTTCTTGGGAGGGAGGTTTTTTTGTGTTGTTTTT
GGGTTTTTTTGGTGTCTTGTGTTTCTTTCTCCTCCATGTGTCTTGGCAGGCACTCATTTCTGT
GGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAGACTCGGGTTGGCTAA
TCCCCGGATGAACGGTGCTCCATTTCGCACCTCCCCTCCTCGTGCCTGCCCTGCCTCTCCACG
CACAGTGTTAAGGAGCCAAGAGGAGCCACTTCGCCCAGACTTTGTTTCCCCACCTCCTGCGG
CATGGGTGTGTCCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTCGCCACCTGG
TCCTTCATGAAGAGCAGACACTTAGAGGCTGGTCCGGAATGGGGAGGTCGCCCCTGGGAGGG
CAGGCGTTGGTTCCAAGCCGGTTCCCGTCCCTGGCGCCTGGAGTGCACACAGCCCAGTCGGC
ACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTTAGAAGGGTCCCC
GCCTTAGATCAATCACGTGGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATG
TCCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTCTGTGTCATTGGATATAATCCTCAGAA
ATAATGCACACTAGCCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACTT
GTAGACTCGGTCACAGTATCAAATAAAATCTATAACAGAAAAAAAAAAAAAAAAA

FIGURE 88

MRQTIKVIKFIILICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
 SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
 RFAVFLSEVSENKLRQLNLNNEWTLDKLRQLTKNAQDKLELHLFMLSIGIPDTVFDLVELEV
 LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRLALHIKFTDIKEIPLWI
 YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
 NNEGTKLIVLNSLKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFO
 HLHRLTCLKLWYNHIAIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKRLRYLDLSHNNLT
 FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRLALHLGNNVLQSLPSRVGELTNLTQIE
 LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain: amino acids 51-75 (type II)

N-glycosylation site: amino acids 262-266, 290-294, 328-332,
 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 amino acids 85-89

Casein kinase II phosphorylation site: amino acids 91-95,
 97-101, 177-181, 253-257, 330-334, 364-368, 398-402, 493-497

N-myristoylation site: amino acids 173-179, 261-267, 395-401,
 441-447

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FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT
 CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT
 GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
 TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGATCAT
 GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGC
 CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
 GTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
 CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
 AATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
 ATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT
 TGCTTGGGTGATTCTTGGATCTCCCCTGTTGATTCGGTGCTCTCCTGGGGACCTTACCTGT
 ACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
 CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
 GATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTAAAAGCACTCCCA
 CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTTCAGCGC
 CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
 GCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA
 TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTTGTGGACGAGTTGCTGGAGGCAGGGATC
 AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCCTG
 GGTGCGGAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGT
 ACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTC
 TACTGGATTCTGAAAGCTGGTCATATGGTTCCCTTCTGACCAAGGGGACATGGCTCTGAAGAT
 GATGAGACTGGTGAATCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT
 TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT
 AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT
 GGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT
 TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

APPROVED	H.O. FIG.	
BY	CLASS	SUBCLASS
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FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKATQR
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNGGLYRE
ATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLORDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMAKMMRLVTQQE

Signal sequence: amino acids 1-25

N-glycosylation site: amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 101-105

Casein kinase II phosphorylation site: amino acids 204-208,
220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site: amino acids 22-28, 76-82, 79-85,
80-86, 119-125, 169-175, 187-193, 195-201, 331-337, 332-338,
360-366

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
T TACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCCATGACATG
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTCGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTCGGCCCAATCGGCCCCGGTGTCTACACCAATATCAGCCACCACTTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCAGCCAGACCCCTCCTGGCCACTACTCTTTTTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGTGTTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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FIGURE 92

MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSRLRW
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNK
LWYQIGVVSWSVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLEFPLLWALPL
LGPV

Signal sequence: amino acids 1-18

N-glycosylation site: amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site: amino acids 86-90,
134-138, 161-165, 190-194, 291-295

N-myristoylation site: amino acids 2-8, 44-50, 101-107,
225-231, 229-235, 239-245, 259-265, 269-275

Amidation site: amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site: amino
acids 252-263,

Serine proteases, trypsin family, histidine active site:
amino acids 78-84

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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FIGURE 93

CCCACGCGTCCGCGGACGCGTGCGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCCTAGGGCT
 CTTTGCCCTCATCCTCTCTGGCAAATGCAGTTACAGCCCGGAGCCCGACCAGCGGAGGACGC
 TGCCCCCAGGCTGGGTGTCCCTGGGCGGTGCGGACCCTGAGGAAGAGCTGAGTCTCACCTTT
 GCCCTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTTCGGATCCCAG
 CTCTCCTCAATACGGAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
 CACTGACCCTCCACACGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCCAGAAGTGCCATTCT
 GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
 TGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC
 ATCCCTACCAGCTTCCACAGGCCTTGGCCCCCATGTGGACTTTGTGGGGGGACTGCACCGT
 TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGCAGGTGACAGGGACTGTAGGCCT
 GCATCTGGGGGTAAACCCCTCTGTGATCCGTAAGCGATACAACTTGACCTCACAAGACGTGG
 GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCTTGAGCAGTATTTCCATGAC
 TCAGACCTGGCTCAGTTCATGCGCCTCTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGC
 CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCGGGATTGAGGCCAGTCTAGATGTGCAGT
 ACCTGATGAGTGCTGGTGCCAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
 GGACAGGAGCCCTTCTGAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
 GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA
 AACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCTGCTCTTCGCCTCAGGTGACAGT
 GGGGCCGGGTGTTGGTCTGTCTCTGGAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAG
 CCCCTATGTCACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTCCTCATCACAAATGAAA
 TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG
 GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC
 CAGTGGCCGTGCCTACCCAGATGTGGCTGCACTTTCTGATGGCTACTGGGTGGTCAGCAACA
 GAGTGCCCATTCATGGGTGTCCGGAACCTCGGCCTCTACTCCAGTGTTTGGGGGGATCCTA
 TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTTGGCTTTCTCAACCCAAG
 GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCTGTCT
 TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCTGGCTGGGATCCTGTAACAGGC
 TGGGGAACACCAACTTCCCAGCTTTGCTGAAGACTCTACTCAACCCCTGACCCTTTCCTATC
 AGGAGAGATGGCTTGTCCTTGCCTGAAGCTGGCAGTTCAGTCCCTTATTCTGCCCTGTTG
 GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCTGAAA
 TGCTGTGAGCTTGACTTGACTCCCAACCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
 CCTGCCTTAGATTCTCAATAAGATGCTGTAAGTAGCATTTTTTGAATGCCTCTCCCTCCGC
 ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGACTA
 TTTCACTTGATATTCATTCCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTTACTCT
 TTCTTACCCTGACATCCAGAAACAATGGCCTCCAGTGCACTTCTCAATCTTTGCTTTATG
 GCCTTTCCATCATAGTTGCCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACCTCTCTG
 ACTACTCTTGCTCTTCTCTCATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCATTGC
 TCCATTTGTAGATTTTTGCTCTTCTCAGTTTACTCATTGTCCCCTGGAACAAATCACTGACA
 TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAAA
 TGTAACAAA

APPROVED	O.C. FIG.	
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FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQONVERLS
 ELVQAVSDPSSPQYGKYLTLNVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
 SIRQAELLPLGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP
 EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
 GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGOEPFLQWLML
 LSNESALPHVHTVSYGDDSDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
 QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
 HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
 RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence: amino acids 1-16

N-glycosylation site: amino acids 210-214, 222-226, 286-290,
 313-317, 443-447

Glycosaminoglycan attachment site: amino acids 361-365,
 408-412, 538-542

Casein kinase II phosphorylation site: amino acids 212-216,
 324-328, 392-396, 420-424, 525-529

N-myristoylation site: amino acids 2-8, 107-113, 195-201,
 199-205, 217-223, 219-225, 248-254, 270-276, 284-290, 409-415,
 410-416, 473-479, 482-488, 521-527, 533-539, 549-555

APPROVED	D.G. FIG.	
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FIGURE 96

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKPKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDELYQQCD
AQP GASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence: amino acids 1-19

N-glycosylation site: amino acids 93-97, 207-211

Glycosaminoglycan attachment site: amino acids 109-113,
316-320

Casein kinase II phosphorylation site: amino acids 77-81,
95-99, 108-112, 280-284, 351-355

N-myristoylation site: amino acids 159-165, 162-168, 202-208,
205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site:
amino acids 171-177

APPROVED	C. G. FIG.	
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FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGGCCCA
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGCTGCCCCACTGTTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAACCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCCTGTGTATTCTTGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCTCAGACCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCC
GGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCGCGGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCCGCCCCCAC
GACTTCCGGCCCCGCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTTAT
AGGTATTTGTAACCCTGCCACATATCTTATTTATTCCTCCAATTTCAATAAATTATTTATT
CTCCAAAAAAAAA

APPROVED	O.G. FIG.	
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FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318

><subunit 1 of 1, 317 aa, 1 stop

><MW: 33732, pI: 7.90, NX(S/T): 1

MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVP IIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC
QVDGAWLLAGIISWGECAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS

Signal sequence: amino acids 1-32

N-glycosylation site: amino acids 62-66, 96-100, 214-218,
382-386, 409-413, 455-459, 628-632, 669-673, 845-849, 927-931,
939-943, 956-960

Glycosaminoglycan attachment site: amino acids 826-830

Casein kinase II phosphorylation site: amino acids 17-21,
39-43, 120-124, 203-207, 254-258, 264-268, 314-318, 323-327,
347-351, 464-468, 548-552, 632-636, 649-653, 671-675, 739-743,
783-787, 803-807, 847-851, 943-947, 958-962, 1013-1017,
1019-1023, 1021-1025

Tyrosine kinase phosphorylation site: amino acids 607-615

N-myristoylation site: amino acids 179-185, 197-203, 320-326,
367-373, 453-459, 528-534, 612-618, 623-629, 714-720, 873-879

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FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCAC
AACAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTCGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTTGCCTTACCTGGTAACTGAGGCCCCATCCTTCCGGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACTTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCCCTATCCCAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG
GGAATCCTACCCCATGCCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG
AGGTCTTGGCCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTTCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACTCAAAGGG
TGAAGAGGTGAGCTGTCTCCTGTGATCTTCCCCACCCTGTCCCCAGCCCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCCTGAGGACTGCACACC
GGGCCCACACCTCTCCTGCCCTCCCTCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCT
CACTGCCTACCTGGCCTGGGGCTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG
TGTAAGCTGGGGATGGGGATTCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTT
TTTGAAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAACCT
GTCCAACCTGTGAAA

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FIGURE 100

MHGSCSFMLLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEE
 LAAFAKAYARQCVWGHNKERRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
 MCGHYTQVWAKTERIGCGSHFCEKLQGVETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC
 PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAEASDSRKMGTTPSSLATGIPAFVLVTEV
 SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS
 THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEAEELPPSSEVLAS
 VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGDPKPSV
 SGLNSGPGHVWGPLLGLLLLLPPLVLGIF

Signal sequence: amino acids 1-22

N-glycosylation site: amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site: amino acids 439-443

Casein kinase II phosphorylation site: amino acids 29-33,
 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site: amino acids 123-129, 143-149, 152-158,
 169-175, 180-186, 231-237, 250-256

Amidation site: amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature: amino acids
 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1:
 amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2:
 amino acids 160-172

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FIGURE 101A

GTAAGTGAAGTCAGGCTTTTCATTTGGGAAGCCCCCTCAACAGAATTCGGTCATTCTCCAAG
TTATGGTGGACGTACTTCTGTTGTTCTCCCTCTGCTTGGCTTTTTCACATTAGCAGACCGGAC
TTAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAGCCTTTCG
AGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGTCTCGGCAA
ATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAA
GAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAACTGC
ATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAAC
CTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAGCTGAACAGGAACCGAATC
TCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAACATCTCGAATTGAACCGAAA
CAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGGTGCTCTGAAGTCTCTGAAAA
TGCAAAGAAATGGAGTAACGAACTTATGGATGGAGCTTTTTGGGGGCTGAGCAACATGGAA
ATTTTGAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCT
GATGCTGCAGGAACCTTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGG
AGTTCTGCCAGAAGCTCAGTGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGAT
TCAAGCTTCCTTGGCCTAAGCTTACTAAATACACTGCACATTGGGAACAACAGAGTCAGCTA
CATTGCTGATTGTGCCTTCCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAACAATG
AAATTTCTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGA
CTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGC
ATTGGAGCATCTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCAC
AAATGAAGAACTGCAACAATTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTA
AAATGGCTCCCACAGTGGGTGGCGGAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGC
CCATCCTCAGCTGCTAAAAGGAAGAAGCATTTTTGCTGTTAGCCCAGATGGCTTTGTGTGTG
ATGATTTTCCCAAACCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTC
AATTTGAGTTTCATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAA
AAAAGACAATGAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAG
GTGGCGAGGTGATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAG
GGGAAATATCAGTGTGTCATCTCAATCACTTTGGTTTATCCTACTCTGTCAAAGCCAAGCT
TACAGTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGG
CCATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAG
GATGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCAGGATGA
CGTGTTCCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGA

Figure 101B

APPROVED	C.G. FIG.	
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FIGURE 101B

From Figure 101A

ACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCCTAGAAACACCATCATTTTTTG
CGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGCATTGCTGG
AGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGTAACCGAGA
GGCACTTTTTTTCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCT
GGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAG
TGTGATCCCCACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCATCGTTAGACGATGACG
GATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGTGTGGTGGGCACGTCACCTC
GTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACCAACAC
AGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCATCTCAGGGAACGTTAGCTG
ACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACCAGTTTGTACATCTTCA
GGTGCTGGATTTTTCTTACCACAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAG
TGAAGCTGATGTGGAAGCTGCCACAGATCTGTTCCCTTTGTCCGTTTTTGGGATCCACAGGCC
CTATGTATTTGAAGGGAAATGTGTATGGCTCAGATCCTTTTGAAACATATCATACAGGTTGC
AGTCCTGACCCAAGAACAGTTTTAATGGACCACTATGAGCCCAGTTACATAAAGAAAAAGGA
GTGCTACCCATGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGT
GGCCTTCACATGTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATG
AAAAATCTGTGTCTAAACAAGTCCTCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGT
TGCCTCGAGTAATTCTTTCATGGGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATG
CCTATTCAAGCTTTGGACAGCCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCAT
TCTTCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGA
AGAAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGT
CTTATGACTTGGACACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAG
TGAACTTTTATTTAAAAGAGAGAGAATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAA
GGATAAAAATGCTTTATTTATACAGATGAACCAAAATTACAAAAGTTATGAAAATTTTTAT
ACTGGGAATGATGCTCATATAAGAATACCTTTTTTAACTATTTTTTTAACTTTGTTTTATGCA
AAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTATAATGC
CAGATTTCTTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTAACA
TTTTTTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATT
TGAA

APPROVED	O.G. FIG.	
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FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRISAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSEKM
QRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE
FCQKLSELDLTFNHL SRLDDSSFLGLSLNLT LHIGNNRVSYIADCAFRGLSSSLKTLDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWL PQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENY AHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDDSPLVVTER
HFFAAGNQLLIIVDSVDSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDDG
WATVGVI IAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNL PADIPSYLSSQGTLD
RQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDFETYHTGCS PDPRTVLMDHYEPSYIKKKECYPCSHPSEESCERSFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEEHNHICTFKQTLNRYRTPNFQS
YDLDT

Signal sequence: amino acids 1-19

Transmembrane domain: amino acids 746-765

N-glycosylation site: amino acids 62-66, 96-100, 214-220,
382-386, 409-413, 455-459, 628-632, 669-673, 845-849, 927-931,
939-943, 956-960

Glycosaminoglycan attachment site: amino acids 826-830

Casein kinase II phosphorylation site: amino acids 17-21,
39-43, 120-124, 203-207, 254-258, 264-268, 314-318, 323-327,
347-351, 464-468, 548-552, 632-636, 649-653, 671-675, 739-743,
783-787, 803-807, 847-851, 943-947, 958-962, 1013-1017,
1019-1023, 1021-1025

Tyrosine kinase phosphorylation site: amino acids 607-615

N-myristoylation site: amino acids 179-185, 197-203, 320-326,
367-373, 453-459, 528-534, 612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTG
 CCTTGCAAAAATGAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAAC
 TGATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGAGCCCTGGATCTTAACACAA
 ATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACAGAGTTAGAGCCGCGGG
 GGTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCCTCCCCACCCCAA
 AAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAAGTATGTTTATTTTT
 CTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTT
 AGTAAAGTAAAGAACTGGTGTGGTGGTGTTCCTTTCTTTTTGAATTTCCCACAAGAGGAG
 AGGAAATTAATAATACATCTGCAAAGAAATTCAGAGAAGAAAAGTTGACCGCGGCAGATTG
 AGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGATTTGTGCCTATGTTGACTAA
 AATTGACGGATAAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTTTTTTTTTAAATTTTTATT
 CCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCTTAACCACCTGGATTTCCATCTGGAT
 GTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAATTCCAGAAGGACCAACACCAGATAAAT
 TATGAATGTTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAAC
 AGGGCCCTATTTGACCCCTGCTTGTGGTGTGCTGGCTCTTCAACTTCTTGTGGTGGCTGG
 TCTGGTGC GGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAACCAGTTCAGCAAGGTGA
 TTTGTGTTCCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCTGCTG
 AACCTCCATGAGAACC AAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTT
 GGAAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTC
 TGGCGAACCTCAACACTCTGGAACCTTTTGACAATCGTCTTACTACCATCCC GAATGGAGCT
 TTTGTATACTTGTCTAAACTGAAGGAGCTCTGGTTGCGAAACAACCCCATTGAAAGCATCCC
 TTCTTATGCTTTTAACAGAATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGAC
 TTTCATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCC
 ATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCT
 TTCTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTTGATGCACCTTCAA
 AACTGTGGATGATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAG
 TCACTAGTGGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCAC
 TCCCTTGCATCATCTAGAGCGGATACATTTACATCACAACCCTTGGAACCTGTAACGTGACA
 TACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTTGTGCCCCG
 TGTAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC
 ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAG
 CTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGA
 ACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGTGCTCAGTGATGGTACGTTAA
 TTTACAAATGTAACGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAATTCGTTG
 GGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCCTTTCTCTTAC
 TTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATA
 CAATGTGGGTCCCCTCCAGTGGTCGACTGGGAGACCACCAATGTGACCACCTCTCTCACAC
 CACAGAGCACAAGGTGACAGAGAAAACCTTCACCATCCCAGTGACTGATATAAACAGTGGG
 ATCCCAGGAATTGATGAGGTCATGAAGACTACCAAATCATCATTGGGTGTTTTGTGGCCAT
 CACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGATGAGGAAGCAGCACCATCGGC
 AAAACCATCACGCCCCAACAAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGA
 GACACACCCATGGAAAGCCACCTGCCCATGCCTGCTATCGAGCATGAGCACCTAAATCACTA
 TAACTCATACAAATCTCCCTTCAACCACACAACAACAGTTAACACAATAAATTC AATACACA
 GTTCAGTGCATGAACCGTTATTGATCCGAATGAACTCTAAAGACAATGTACAAGAGACTCAA
 ATCTAAACATTTACAGAGTTACAAAAACAAACAATCAAAAAAAGACAGTTTATTAAAA
 ATGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGCTTTACAAAAAACAAAA
 AAGAAAAGAAATTTATTTATTAAAAATTCTATTGTGATCTAAAGCAGACAAAAA

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FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGI STNTRLLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNPNIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDSLGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQD TGMYTCMVNSVGN
TTASATLNVTAATTTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTS LTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence: amino acids 1-44

Transmembrane domain: amino acids 523-543

N-glycosylation site: amino acids 278-282, 364-368, 390-394,
412-416, 415-419, 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 183-187

Casein kinase II phosphorylation site: amino acids 268-272,
417-421, 465-469, 579-583, 620-624

N-myristoylation site: amino acids 40-46, 73-79, 118-124,
191-197, 228-234, 237-243, 391-397, 422-428, 433-439, 531-537

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FIGURE 105A

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCCTG
 CTGTTTGGGGGCATGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCG
 CGAGGGAGGAGCGCGCACGCGACCGCGAGGGCGGGCGTGACCCCTCGGCTGGAAGTTTGTGC
 CGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGAGACCTAGGCCGCTGGACCGCGAT
GAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTTGGGGCTGCTGCTGTGCGCGGTGCTGG
GGCGCGCTGGCCGGTCCGACAGCGCGGTGCGGGGAACTCGGGCAGCCCTCTGGGGTAGCC
 GCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTGGACTGCAGTCGTAA
 GCGGCTAGCGCGTCTTCCCAGGCCACTCCCGTCTGGGTGCTCGGCTGGACTTAAGTCACA
 ACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAGCCTTCGAGAAGTGAAA
 CTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGTCTCGGCAAATATTACACT
 TCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAGTTTCAGT
 CCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTAGAGCTCCAAACTGCATTTCCAGCC
 CTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTT
 TGACAATTTGGCCAACACACTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCC
 CACCCAAGATGTTTAAACTGCCCCAACTGCAACATCTCGAATTGAACCGAAACAAGATTAAA
 AATGTAGATGGACTGACATTCCAAGGCCTTGGTGCTCTGAAGTCTCTGAAAATGCAAAGAAA
 TGGAGTAACGAAACTTATGGATGGAGCTTTTTGGGGGCTGAGCAACATGGAAATTTTGCAGC
 TGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAG
 GAACTTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCA
 GAAGCTCAGTGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCC
 TTGGCCTAAGCTTACTAAATACACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGAT
 TGTGCCTTCCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTTG
 GACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCC
 AAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCAT
 CTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAA
 ACTGCAACAATTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCC
 CACAGTGGGTGGCGGAAAACAACCTTTAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAG
 CTGCTAAAAGGAAGAAGCATTTTTGCTGTTAGCCAGATGGCTTTGTGTGTGATGATTTTCC
 CAAACCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTT
 TCATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAGACAAT
 GAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCCAAGGTGGCGAGGT

_____ To Figure 105B

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FIGURE 105B

From Figure 105A

GATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATC
AGTGTGTCATCTCCAATCACTTTGGTTCATCCTACTCTGTCAAAGCCAAGCTTACAGTAAAT
ATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCCATGGCAGC
CTTGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGGCA
CAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCAGGATGACGTGTTCTTT
ATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGG
AAGTATTTTACGCAAATGCAACTCTGACTGTCCTAGAAACACCATCATTTTTTGGGCCACTGT
TGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGCATTGCTGGAGGAAGCCCT
CCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGTAACCGAGAGGCACTTTTT
TGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGGAAATACA
CATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCC
ACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCAC
TGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGTGTGGTGGGCACGTCACCTCGTGTGGGTGG
TCATCATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACCAACACAGATGAGACC
AACTTGCCAGCAGATATTCCTAGTTATTTGTCATCTCAGGGAACGTTAGCTGACAGGCAGGA
TGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACCAGTTTGTACATCTTCAGGTGCTGGAT
TTTTCTTACCACAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGAT
GTGGAAGCTGCCACAGATCTGTTCCCTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTT
GAAGGGAAATGTGTATGGCTCAGATCCTTTTGAAACATATCATACAGGTTGCAGTCCTGACC
CAAGAACAGTTTTTAATGGACCACTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCA
TGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACA
TGTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGT
GTCTAAACAAGTCCTCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGT
AATTCTTTTCATGGGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAG
CTTTGGACAGCCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAG
ACTTGGA CTCTGGGTGAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCAC
ATTTGTACCTTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTT
GGACACA TAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACTTTTA
TTTAAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAT
GCTTTATTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTTTATACTGGGAATG
ATGCTCATATAAGAATACCTTTTTTAAACTATTTTTTAACTTTGTTTTATGCAAAAAAGTATC
TTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTTATAATGCCAGATTTCTT
TTTATGGAAAATGAGTTACTAAAGCATTTTTAAATAATACCTGCCTTGTAACATTTTTTTAAAT
AGAAGTTACTTCATTATATTTTGCACATTATTTTAAATAAATGTGTCAATTTGAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGDLLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRI SAIPPKMFKL PQLOHLELN RNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC
QKLSELDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLOGNAFSQMK
KLQQHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDE
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAH LRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGH PAPQIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNWTKDDSPLVVTERHF
FAAGNQLLLIIVDSVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDDGWA
TVGVVIIIAVCCVVGTSLVWVVI IYHTRRRNEDCSITNTDETNPADIPSYLSSQGT LADRQ
DGYVSSSESGSHHQFVTSSGAGFFLPQH DSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKG NVYGSDPFETYHTGCSPDPRTV LMDHYEPSYIKKKECYPCHPSEESCERSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYD
LDT

Signal sequence: amino acids 1-27

Transmembrane domain: amino acids 808-828

N-glycosylation site: amino acids 122-126, 156-160, 274-278,
442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991,
999-1003, 1016-1020

Glycosaminoglycan attachment site: amino acids 886-890

Casein kinase II phosphorylation site: amino acids 99-103,
180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411,
524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847,
863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083,
1081-1085

Tyrosine kinase phosphorylation site: amino acids 667-675

N-myristoylation site: amino acids 14-20, 36-42, 239-245,
257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687,
774-780, 933-939

Leucine zipper pattern: amino acids 58-80, 65-87

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FIGURE 107A

CAAAACTTGCCTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGA
 GCGCAGCTGAGACTGGGGGAGCGCGTTTCGGCCTGTGGGGCGCCGCTCGGCGCCGGGGCGCAG
 CAGGGAAGGGGAAGCTGTGGTCTGCCCTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGA
 GCCCCTGGGTGGTCCCGTCCCCTATCCCTCCTTTATATAGAAACCTTCCACACTGGGAAGGC
 AGCGGCGAGGCAGGAGGGCTCATGGTGAGCAAGGAGGCCGCTGATCTGCAGGCGCACAGCA
 TTCCGAGTTTACAGATTTTTACAGATACCAAATGGGAAGGCGAGGAGGCAGAACAGCCTGCCT
 GGTTCATCAGCCCTGGCGCCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCC
 CAGAGCCGGGTGCTGCTGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCT
 TGCCGTGAGGGCCCCAGGATTTGGCCGAAGTGGCGGCCACAGCCTGAGCCCCGAAGAGAACG
 AATTTGCGGAGGAGGAGCCGGTGTGGTACTGAGCCCTGAGGAGCCCGGGCCTGGCCCAGCC
 GCGGTCAGCTGCCCCCGAGACTGTGCCTGTTCCCAGGAGGGCGTCGTGGACTGTGGCGGTAT
 TGACCTGCGTGAGTTCCCGGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGCAGAAC
 ACCAGCTGGAAAAGATCTACCCTGAGGAGCTCTCCCGGCTGCACCGGCTGGAGACACTGAAC
 CTGCAAAACAACCGCCTGACTTCCCGAGGGCTCCCAGAGAAGGCGTTTGAGCATCTGACCAA
 CCTCAATTACCTGTACTTGGCCAATAACAAGCTGACCTTGGCACCCCGCTTCCTGCCAAACG
 CCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAAGATCTATGGGCTCACCTTTGGC
 CAGAAGCCAAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGGCAGACGCCGGGCTGCC
 GGACAACATGTTCAACGGCTCCAGCAACGTCGAGGTCCTCATCCTGTCCAGCAACTTCCTGC
 GCCACGTGCCCAAGCACCTGCCGCTGCCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTG
 GAGAAGATCCCCCGGGGGCCTTCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAA
 CAACTACCTGACTGACGAGGGCCTGGACAACGAGACCTTCTGGAAGCTCTCCAGCCTGGAGT
 ACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGGCTGCCGCGCAGCCTGGTG
 CTGCTGCACTTGGAGAAGAACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCCG
 CAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCCACTGG
 CCTTCCAGGGCCTCAAGCGGTTGCACACGGTGCACCTGTACAACAACGCGCTGGAGCGCGTG
 CCCAGTGGCCTGCCTCGCCGCTGCGCACCCCTCATGATCCTGCACAACCAGATCACAGGCAT
 TGGCCGCGAAGACTTTGCCACCACCTACTTCTGGAGGAGCTCAACCTCAGCTACAACCGCA
 TCACCAGCCCACAGGTGCACCGCGACGCCTTCCGCAAGCTGCGCCTGCTGCGCTCGCTGGAC
 CTGTGCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAA
 GGTCAAGCGCAATGAGCTGGCTGCCTTGGCACGAGGGGCGCTGGCGGGCATGGCTCAGCTGC
 GTGAGCTGTACCTCACCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCGTGCCTGGGTG

_____ To Figure 107B

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FIGURE 107B

From Figure 107A

GACCTCGCCCATCTGCAGCTGCTGGACATCGCCGGGAATCAGCTCACAGAGATCCCGGAGGG
GCTCCCGAGTCACTTGAGTACCTGTACCTGCAGAACACAAGATTAGTGCGGTGCCCGCCA
ATGCCTTCGACTCCACGCCAACCTCAAGGGGATCTTTCTCAGGTTTAACAAGCTGGCTGTG
GGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGACATTGAAGG
CAACTTAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAAGGAGGAGG
AGGAAGAGGAGGAGGAGGAGGAAGAGGAAACAAGATTAGTGACAAGGTGATGCAGATGTGACC
TAGGATGATGGACCGCCGGACTCTTTTCTGCAGCACACGCCTGTGTGCTGTGAGCCCCCAC
TCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCATCCACATGACACGGGCT
GACACAGTCTCATATCCCCACCCCTTCCCACGGCGTGTCCACGGCCAGACACATGCACACA
CATCACACCCTCAAACACCCAGCTCAGCCACACACAACCTACCCTCCAAACCACCACAGTCTC
TGTCACACCCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAGGGTCTGCCCTGC
CCTGGCACACACAGGCACCCATTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACA
CCACACACACACATGCACAAGTCATGTGCGAACAGCCCTCCAAAGCCTATGCCACAGACA
GCTCTTGCCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCTGTCCATCTGTCCGTC
CGTTCCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCCTCTGG
AACTCACAAAAGCTGGCTTTTATTCTTTTCCCATCCTATGGGGACAGGAGCCTTCAGGACTG
CTGGCCTGGCCTGGCCACCCCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCC
TCCCTGCCACGCCCTGGCAGGACACAGGCACCTTTTCCAATGGGCAAGCCCAGTGGAGGCAGG
ATGGGAGAGCCCCCTGGGTGCTGCTGGGGCCTTGGGGCAGGAGTGAAGCAGAGGTGATGGGG
CTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTTTGTTCTTCAGGCC
TGTGGGGGAAGTTCCGGGTGCCTTTATTTTTTATTCTTTTCTAAGGAAAAAATGATAAAAA
TCTCAAAGCTGATTTTTCTTGTTATAGAAAACTAATATAAAAGCATTATCCCTATCCCTGC
AAAAAAAAA

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FIGURE 108

MEGEEAEQPAWFHQPWPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSP EENEF AEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVDCGGIDLREFPGDLP
EHTNHLSQLNNQLEKIYPEELSRHLRLETNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMLHNNQITGIGREDFATTYF
LEELNLSYNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEEETR

Signal sequence: amino acids 1-48

N-glycosylation site: amino acids 243-247, 310-314, 328-332, .
439-443

Casein kinase II phosphorylation site: amino acids 68-72,
84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site: amino acids 19-25, 107-113, 213-219,
217-223, 236-242, 335-341, 477-483, 498-502, 539-545, 548-554

Leucine zipper pattern: amino acids 116-138, 251-273,
258-280, 322-344, 464-486, 471-493, 535-557

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FIGURE 109A

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCCT
CCGGGAGCGGCAGCAGTAGCCCCGGGCGGCGAGGGCTGGGGGTTCCTCGAGACTCTCAGAGGG
GCGCCTCCCATCGGGCGCCACCACCCCAACCTGTTCCCTCGCGCGCCACTGCGCTGCGGCCCA
GGACCCGCTGCCCAACATGGATTTTCTCCTGGCGCTGGTGCTGGTATCCTCGCTCTACTGC
AGGCGGCCCGCCGAGTTCGACGGGAGGTGGCCCAGGCAAATAGTGTCATCGATTGGCCTATGT
CGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTC
GCCTGTGTGCCAACCACGATGCAAACATGGTGAATGTATCGGGCCAAACAAGTGCAAGTGTC
ATCCTGGTTATGCTGGAAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGG
CCCTGTAAGCACAGGTGCATGAACACTTACGGCAGCTACAAGTGCTACTGTCTCAACGGATA
TATGCTCATGCCGGATGGTTCCCTGCTCAAGTGCCCTGACCTGCTCCATGGCAAACCTGTCAGT
ATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCCTGGCCTGCACCTG
GCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCCTGCCC
TAGATTTAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTCATAAAGGCTTCG
ATCTCATGTATATTGGAGGCAAATATCAATGTCATGACATAGACGAATGCTCACTTGGTCAG
TATCAGTGCAGCAGCTTTGCTCGATGTTATAACGTACGTGGGTCCCTACAAGTGCAAATGTAA
AGAAGGATACCAGGGTGATGGACTGACTTGTGTGTATATCCCAAAGTTATGATTGAACCTT
CAGGTCCAATTCATGTACCAAAGGGAAATGGTACCATTTTAAAGGGTGACACAGGAAATAAT
AATTGGATTCCCTGATGTTGGAAGTACTTGGTGGCCTCCGAAGACACCATATATTCCTCCTAT
CATTACCAACAGGCCTACTTCTAAGCCAACAACAAGACCTACACCAAAGCCAACACCAATTC
CTACTCCACCACCACCACCACCCCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACC
CCAGAAAGGCCAACCACCGGACTGACAACTATAGCACCAGCTGCCAGTACACCTCCAGGAGG
GATTACAGTTGACAACAGGGTACAGACAGACCCTCAGAAACCCAGAGGAGATGTGTTCAAGT
TTCTGGTACACAGTTGTAATTTTGACCATGGACTTTGTGGATGGATCAGGGAGAAAGACAAT
GACTTGCACTGGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGCGGCAGC
CAAAGCCCCAGGGGGAAAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCCTCATGCATTCAG
GGGACCTGTGCCTGTCATTCAGGCACAAGGTGACGGGGCTGCACTCTGGCACACTCCAGGTG
TTTGTGAGAAAACACGGTGCCACGGAGCAGCCCTGTGGGGAAGAAATGGTGGCCATGGCTG
GAGGCAAACACAGATCACCTTGCAGGGGGCTGACATCAAGAGCGAATCACAAAGATTGATTAA
AGGGTTGGAAAAAAGATCTATGATGGAAAATTAAAGGAACCTGGGATTATTGAGCCTGGAGA
AGAGAAGACTGAGGGGCAAACCATTGATGGTTTTCAAGTATATGAAGGGTTGGCACAGAGAG

_____ To Figure 109B

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FIGURE 109B

From Figure 109A

GGTGGCGACCAGCTGTTCTCCATATGCACTAAGAATAGAACAAGAGGAAACTGGCTTAGACT
AGAGTATAAGGGAGCATTTCTTGGCAGGGGCCATTGTTAGAATACTTCATAAAAAAAGAAGT
GTGAAAATCTCAGTATCTCTCTCTCTTTCTAAAAAATTAGATAAAAATTTGTCTATTTAAGA
TGGTTAAAGATGTTCTTACCCAAGGAAAAGTAACAAATTATAGAATTTCCCAAAGATGTTT
TGATCCTACTAGTAGTATGCAGTGAAAATCTTTAGAACTAAATAATTTGGACAAGGCTTAAT
TTAGGCATTTCCCTCTTGACCTCCTAATGGAGAGGGATTGAAAGGGGAAGAGCCCACCAAAT
GCTGAGCTCACTGAAATATCTCTCCCTTATGGCAATCCTAGCAGTATTAAAGAAAAAAGGAA
ACTATTTATTCCAAATGAGAGTATGATGGACAGATATTTTAGTATCTCAGTAATGTCCTAGT
GTGGCGGTGGTTTTTCAATGTTTCTTCATGGTAAAGGTATAAGCCTTTCATTTGTTCAATGGA
TGATGTTTCAGATTTTTTTTTTTTTTAAGAGATCCTTCAAGGAACACAGTTCAGAGAGATTTT
CATCGGGTGCAATTCTCTCTGCTTCGTGTGTGACAAGTTATCTTGGCTGCTGAGAAAGAGTGC
CCTGCCCCACACCGGCAGACCTTTCCTTCACCTCATCAGTATGATTCAGTTTCTCTTATCAA
TTGGACTCTCCCAGGTTCCACAGAACAGTAATATTTTTTTGAACAATAGGTACAATAGAAGGT
CTTCTGTCATTTAACCTGGTAAAGGCAGGGCTGGAGGGGGGAAATAAATCATTAAGCCTTTG
AGTAACGGCAGAATATATGGCTGTAGATCCATTTTTAATGGTTCATTTCCCTTTATGGTCATA
TAACTGCACAGCTGAAGATGAAAGGGGAAAATAAATGAAAATTTTACTTTTCGATGCCAATG
ATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTTGTTTATTA
TTTAATGTTTTCTAAAATAAAAAATGTTAGTGGTTTTCCAAATGGCCTAATAAAAACAATTA
TTTGTAATAAAAACACTGTTAGTAAT

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FIGURE 110

MDFLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
 RCKHGEICIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
 GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCDVDVDECATGRASCPRFRQC
 VNTFGSYICKCHKGFDLMYIGGKYQCHDIDEC SLGQYQCSSFARCYNVRGSYKCKCKEGYQG
 DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGD TGNNNWIPDVGSTWWPPKTPYIPPIITNRP
 TSKPTTRPTPKPTPIPTPPPPPLPTLRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDN
 RVQTD PQKPRGDVFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAKAPGG
 KAARLVLPGLRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
 TLRGADIKSESQR

Signal sequence: amino acids 1-17

N-glycosylation site: amino acids 273-277

Casein kinase II phosphorylation site: amino acids 166-170,
345-349

Tyrosine kinase phosphorylation site: amino acids 199-206

N-myristoylation site: amino acids 109-115, 125-131, 147-153,
191-197, 221-227, 236-242, 421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site: amino acids
104-116, 186-198, 231-243

Cell attachment sequence: amino acids 382-385

EGF-like domain cysteine pattern signature: amino acids 75-87

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FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCCTTTAGATTGTGA
 AATGTGGCTCAAGGTCTTCACAACTTTCCTTTCCCTTTGCAACAGGTGCTTGCTCGGGGCTGA
 AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTC
 CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA
 CACAATGCCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAATACC
 AACACAAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCT
 GATGAAGGCAATTACATCGTGAAGGTCAACATTCAGGGAAATGGAACCTCTATCTGCCAGTCA
 GAAGATACAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTCATCCTCCCT
 CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGG
 CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
 TCCCCAAAACAATACCCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
 GCCTGGTGAGGAACCCCTGTCAGTGAAATGGAAAGTGATATCATTATGCCCATCATATATTAT
 GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGTGTTTACTGT
 TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
 CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCCTCGCTTAGAAGTT
 GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
 CGGCAGGCAAGATGAAACTCATTTCACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG
 CACAGAAAGGAAAATCATTGTACCTTTAGCAAGTATAACTGGAATATCACTATTTTTTGATT
 ATATCCATGTGTCTTCTCTTCCTATGGAAAAAATATCAACCCACAAAGTTATAAAACAGAA
 ACTAGAAGGCAGGCCAGAAACAGAAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG
 CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTCAGG
 ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT
 GTATGAAGTTATTACGCATCCCTGCCAGCAGCAAGACCATCCAGAGTGAACCTTTTCATGG
 GCTAAACAGTACATTTCGAGTGAAATTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAGT
 ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCCTTTACA
 TGCAGAATAGAGGCATTTATGCAAATTGAACTGCAGGTTTTTCAGCATATACACAATGTCTT
 GTGCAACAGAAAAACATGTTGGGGAAATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
 GGAGAACGAAAGTGACAGGGGTTTCCTCATAAGTTTTGTATGAAATATCTCTACAAACCTCA
 ATTAGTTCTACTCTACACTTTCACATATCAACACTGAGACTATCCTGTCTCACCTACAAA
 TGTGGAACTTTACATTGTTTCGATTTTTTCAGCAGACTTTGTTTTATTAAATTTTTATTAGTG
 TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTTATTTGTACAA
 CAAAGTAATAAGGATGGTTGTCACAAAAACAAACTATGCCTTCTCTTTTTTTTCAATCACC
 AGTAGTATTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTA
 TTTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTTTGCTTTTAAAAAATAAA
 AA

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FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVGRQALYLPVHYGFHTPASDIQIIWLFERPHTMP
 KYLLGSVNKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTLSASQKIQVTV
 DDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSTSPQNNTLHIA
 PVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTVDLGEAILFDCSA
 DSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNITGRQDETHETVIITSV
 GLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQKLEGRPETEYRKAQTFSGH
 EDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTVYEVIQHIPAQQQDHPE

Signal sequence: amino acids 1-18

Transmembrane domain: amino acids 341-359

N-glycosylation site: amino acids 73-77, 92-96, 117-121,
 153-157, 189-193, 204-208, 276-280, 308-312

Casein kinase II phosphorylation site: amino acids 129-133,
 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site: amino acids 272-280

N-myristoylation site: amino acids 15-21, 19-25, 118-124,
 163-167, 203-209, 231-237, 239-245

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 7-18

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FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGACAGTTCCTGGCAGTCCTGGTGGTGT
GCTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCT
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGGAGAAGATCTTGAGGTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC
TTCCTACTATTTATCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGCCCGTTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT
GTTTTTGCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC
AGATTGCCTTTGTCCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCTTCAAAAAAAT
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAGACTTTCCACAGAATGC
CATAAGACAACGCTCTCTGGGTCCATCATTTGGCCACAGATAAATCCTAGTTAAATTTTATAG
TTATCTTAATATTATGATTTTGATAAAAACAGAAGATTGATCATTTTGTGGTTTGAAGTG
AACTGTGACTTTTTTGAATATTGCAGGGTTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA
CATTGAGAACATAAAAGCACTAGGTATACAAGTTTGAATATGATTTAAGCACAGTATGATG
GTTTAAATAGTTCTCTAATTTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGT
TTAATAATAACCTATTTCAAGTCTGAGTTTTGAAAATTTACATTTCCCAAGTATTGCATTAT
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTCTCTG
TTTCACTGTGTGAAAAAAGAAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGTCTCAAG
AAATGTGTATTTTCAGTGACAATTTCTGGTCTTTTTTAGAGGTATATTCCAAAATTTCTTGT
ATTTTTAGGTTATGCAACTAATAAAAACCTTACATTAATTAATTACAGTTTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATTC
CAACAAAGTTTGATTTTCTCTTGATTTTTTCTTACTTACTATGGGTACATTTTTTTATTTTT
CAAATTGGATGATAATTTCTTGAAACATTTTTTATGTTTTAGTAAACAGTATTTTTTTGTT
GTTTCAAAGTGAAGTTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTTAAATTT
TTGGCCACTTTTTTCAGATTTTACATCATTCTTGCTGAACTTCAACTTGAAATTTGTTTTTT
TTTCTTTTTGGATGTGAAGGTGAACATTCCTGATTTTTGTCTGATGTGAAAAAGCCTTGGA
TTTTACATTTTGAAATTCAAAGAAGCTTAATATAAAAGTTTGCACTTACTCAGGAAAAAG
CATCTTCTTGATATATGCTTAAATGTATTTTTGTCTCATATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTTGATGTTTTAAATAATAACATTTTTATATTTTTTAAAGACAA
ACTTCATATTATCCTGTGTTCTTTCCTGACTGGTAATATTGTGTGGGATTTTCACAGGTAAAA
GTCAGTAGGATGGAACATTTTAGTGTATTTTTACTCCTTAAAGAGCTAGAATACATAGTTTT
CACCTTAAAGAAGGGGGGAAAATCATAAATAAATGAATCAACTGACCATTACGTAGTAGAC
AATTTCTGTAATGTCCCCTTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG
TATCGTAATATAAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAATATTGTACCATT
AAAGAGTTTGGATGTGTAACCTTGTGATGCCTTAGAAAAATATCCTAAGCACAAAATAAACCT
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAAAAAAAA

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FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEEQEAEDEEDVSE
EEAESKEGTNKDFPQNAIRQRS LGPSLATDKS

Signal sequence: amino acids 1-26

Transmembrane domain: amino acids 182-201

Casein kinase II phosphorylation site: amino acids 68-72,
119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site: amino acids 107-115

N-myristoylation site: amino acids 20-26, 192-198

Amidation site: amino acids 25-29

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FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTTAACTAATTCAACAAACGGGACCCCTT
 CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCAGTGGGACAGGCGGATTGGAAGAGCGGG
 AAGGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCAATGAAACTCTGGGTGTCTGC
 ATTGCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATTCTTCACCTCTATTG
 GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
 CTTGTGGAGGAAGCCAAGCTTTCAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC
 TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAACTGG
 TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
 GGTTTTATCGCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGG
 AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA
 GAGGGGAACTTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
 GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT
 AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
 GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCCTGCTC
 TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA
 GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCA
 TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCGTGGG
 GAGGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA
 CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA
 TCGTCAGGTACTACGATGTCATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
 CCTAAACTTGCACGAGCCACCGTTCGTGATCCCAAGACAGGAGTCTCACTGTGCGCCAGCTA
 CCGGGTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCTGTTGTGGCCCGAGTAAATC
 GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTGCAAAT
 TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGG
 CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGATGTAGAAGCTG
 GTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG
 TTCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAAGACATGCTGCCTGCCC
 TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT
 TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTTTCTGTCTTCCCCTTCCTGGTC
 CTTACGCCCATGTCAACGTGACAGACACCTTTGTATGTTCTTTGTATGTTTCTATCAGGCT
 GATTTTTTGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
 GTGACTGAAGTCCCAGCCCTTCCATTCAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
 AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTTGTACCTCAGGTGTT
 TTAGGTGTGAGATGTTTCAGTGAACCAAAGTTCTGATACCTTGTTTACATGTTTGTTTTTAT
 GGCATTTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAAAA

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FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
 NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFP
 TDEDEIGAALKMRLQDQTYRLDPGTISRGEPLPGTKYQAMLSVDDCFGMGRSAYNEGDYYHTV
 LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
 YFEQLLEEEREKTLTNQTEAELATPEGIYERPVLDYLPERDVYESLCRGEGVKLTERRQKRLF
 CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYDVMSEEEIERIKEIAKPKLARATVRDPKTG
 VLTVASYRVSKSSWLEEDDDPVVARVNRMRQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
 RRPFDGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGECDYR
 TRHAACPVLVGCKWVS NKWFHERGQEFRLPCGSTVD

Signal sequence: amino acids 1-17

N-glycosylation site: amino acids 115-119, 264-268

Glycosaminoglycan attachment site: amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 amino acids 477-481

Casein kinase II phosphorylation site: amino acids 43-47,
 72-76, 125-129, 151-155, 165-169, 266-270, 346-350, 365-369,
 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site: amino acids 71-80,
 489-496

N-myristoylation site: amino acids 14-20, 131-137, 171-177,
 446-452

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 8-19

Leucine zipper pattern: amino acids 213-235

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FIGURE 117

GCAGTATTGAGTTTTACTTCCTCCTCTTTTTAGTGGAAGACAGACCATAATCCCAGTGTGAG
TGA AATTGATTGTTTCATTTATTACCGTTTTGGCTGGGGGTTAGTTCCGACACCTTCACAGT
TGAAGAGCAGGCAGAAGGAGTTGTGAAGACAGGACAATCTTCTTGGGGATGCTGGTCCCTGGA
AGCCAGCGGGCCTTGCTCTGTCTTTGGCCTCATTGACCCAGGTTCTCTGGTTAAAACTGAA
AGCCTACTACTGGCCTGGTGCCCATCAATCCATTGATCCTTGAGGCTGTGCCCCCTGGGGCAC
CCACCTGGCAGGGCCTACCACCATGCGACTGAGCTCCCTGTTGGCTCTGCTGCGGCCAGCGC
TCCCCCTCATCTTAGGGCTGTCTCTGGGGTGCAGCCTGAGCCTCCTGCGGGTTTTCTGGATC
CAGGGGGAGGGAGAAGATCCCTGTGTGCGAGGCTGTAGGGGAGCGAGGAGGGGCCACAGAATCC
AGATTCGAGAGCTCGGCTAGACCAAAGTGATGAAGACTTCAAACCCCGGATTGTCCCCTACT
ACAGGGACCCCAACAAGCCCTACAAGAAGGTGCTCAGGACTCGGTACATCCAGACAGAGCTG
GGCTCCCGTGAGCGGTTGCTGGTGGCTGTCTTGACCTCCCGAGCTACACTGTCCACTTTGGC
CGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTCGGTTACTCTACTTCACTGGGCAGC
GGGGGGCCCGGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGGATGAGCGGCCCGCCTGG
CTCATGTGAGAGACCCTGCGCCACCTTCACACACACTTTGGGGCCGACTACGACTGGTTCTT
CATCATGCAGGATGACACATATGTGCAGGCCCCCGCCTGGCAGCCCTTGCTGGCCACCTCA
GCATCAACCAAGACCTGTACTTAGGCCGGGCAGAGGAGTTTATTGGCGCAGGCGAGCAGGCC
CGGTACTGTGATGGGGGCTTTGGCTACCTGTTGTACGGAGTCTCCTGCTTCGTCTGCGGCC
ACATCTGGATGGCTGCCGAGGAGACATTCTCAGTGCCCGTCTGACGAGTGGCTTGACGCT
GCCTCATTGACTCTCTGGGCGTCGGCTGTGTCTCACAGCACCAGGGGCAGCAGTATCGCTCA
TTTGAACCTGGCCAAAATAGGGACCCTGAGAAGGAAGGGAGCTCGGCTTTCCTGAGTGCCTT
CGCCGTGCACCCTGTCTCCGAAGGTACCCTCATGTACCGGCTCCACAAACGCTTCAGCGCTC
TGGAGTTGGAGCGGGCTTACAGTGAAATAGAACAACCTGCAGGCTCAGATCCGGAACCTGACC
GTGCTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCCTTTCAC
ACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGCACACCTTCTCCT
GTGCAGATGGGGCTCCCAAGTGCCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCG
TTGGAGACTGCCCTGGAGCAGCTCAATCGGCGCTATCAGCCCCGCTGCGCTTCAGAAAGCA
GCGACTGCTCAACGGCTATCGGCGCTTCGACCCAGCACGGGGCATGGAGTACACCCTGGACC
TGCTGTTGGAATGTGTGACACAGCGTGGGCACCGGCGGGCCCTGGCTCGCAGGGTCAGCCTG
CTGCGGCCACTGAGCCGGGTGGAAATCCTACCTATGCCCTATGTCACTGAGGCCACCCGAGT
GCAGCTGGTGTGCCACTCCTGGTGGCTGAAGCTGCTGCAGCCCCGGCTTTCCTCGAGGCGT
TTGCAGCCAATGTCTTGAGCCACGAGAACATGCATTGCTCACCTGTTGCTGGTCTACGGG
CCACGAGAAGGTGGCCGTGGAGCTCCAGACCCATTTCTTGGGGTGAAGGCTGCAGCAGCGGA
GTTAGAGCGACGGTACCCTGGGACGAGGCTGGCCTGGCTCGCTGTGCGAGCAGAGGCCCTT
CCCAGGTGCGACTCATGGACGTGGTCTCGAAGAAGCACCCCTGTGGACACTCTCTTCTTCCTT
ACCACCGTGTGGACAAGGCCTGGGCCCCGAAGTCTCAACCGCTGTCGCATGAATGCCATCTC
TGGCTGGCAGGCCTTCTTTCCAGTCCATTTCCAGGAGTTCAATCCTGCCCTGTACCCACAGA
GATCACCCCCAGGGCCCCCGGGGGCTGGCCCTGACCCCCCTCCCTCCTGGTGTGACCCC
TCCCGGGGGGCTCCTATAGGGGGGAGATTTGACCGGCAGGCTTCTGCGGAGGGCTGCTTCTA
CAACGCTGACTACCTGGCGGCCCGAGCCCGGCTGGCAGGTGAACTGGCAGGCCAGGAAGAGG
AGGAAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTTCTCCGGTTCTCAGGGCTCCACCTC
TTTCGGGCCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCCACGGCT
CAGTGAAGAACTCTACCACCGCTGCCGCTCAGCAACCTGGAGGGGCTAGGGGGCCGTGCCC
AGCTGGCTATGGCTCTCTTTGAGCAGGAGCAGGCCAATAGCACTTAGCCCGCCTGGGGGCC
TAACCTCATTACCTTTCTTTGTCTGCCTCAGCCCCAGGAAGGGCAAGGCAAGATGGTGGAC
AGATAGAGAATTGTTGCTGTATTTTTTAAATATGAAAATGTTATTAAACATGTCTTCTGCC

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FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
 QSDEDFKPRIVPYRDPNKPYPYKVLTRYIQTELGSRRERLLVAVLTSRATLSTLAVAVNRTV
 AHHFPRLLYFTGQRGARAPAGMQVVS HGDERP AWMSETLRHLHTHFGADYDWWFFIMQDDTY
 VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
 DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
 GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEV
 LGWDYFTEQHTFSCADGAPKCP LQGASRADVGDALETALEQLNRRYQPRLR FQKQRL LN GYR
 RFD PARGMEYTLDLLLEC VTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLP LL
 VAEAAAAPAFLEAFAANVLEPREHALLTLLL VYGPREGGRGAPDPFLGVKAAA AE LERRY PG
 TRLAWLAVRAEAPSQVRLMDVVS KKHVPD TLFFLT TVWTRPGPEVLNRCRMNAISGWQAFFP
 VHFQEFNPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
 RARLAGELAGQEEEEALEGLEVMDFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
 CRLSNLEGLGGRAQLAMALFEQE QANST

Signal sequence: amino acids 1-15

Transmembrane domain: amino acids 489-507

N-glycosylation site: amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 amino acids 319-323, 464-468

Casein kinase II phosphorylation site: amino acids 64-68,
 150-154, 322-326, 331-337, 368-372, 385-389, 399-403, 409-413,
 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site: amino acids 736-743

N-myristoylation site: amino acids 19-25, 23-29, 136-142,
 397-403, 441-447, 544-550, 558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 14-25

Cell attachment sequence: amino acids 247-250

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FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAACC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTTTGAGTCAATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACCTG
GTTCTTCCTTGACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTTGAGATATGGCTGTTACTTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTGTTGGGCATATTTTCAAT
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTTGAAGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACCTACATATCCAA
TACAGCTGTATGTTTCTTTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTTTTAAATGAGGGTGGTTTTTTTCTTTTAAACACATGAACATTGTAAATG
TGTTGGAAGAAGTGTTTTAAGAATAATAATTTTGCAAATAAACTATTAATAAATATTATAT
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTGTGATTGGTT
AAAAAATTTTAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTTGCCTTCTCAAAATGTACAACCTAAGCAACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAAT

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FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
 LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK
 AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG
 IVLSVESMKRLNSLLNIPEKCPEQGGMWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
 KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMYGVYRLRAFGHIFNDALVEL
 PPNGSDND

Signal sequence: amino acids 1-33

N-glycosylation site: amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 amino acids 319-323, 464-468

Casein kinase II phosphorylation site: amino acids 64-132,
 150-154, 322-326, 331-335, 368-372, 385-389, 399-403, 409-413,
 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site: amino acids 736-743

N-myristoylation site: amino acids 19-25, 23-29, 136-142,
 397-403, 441-447, 544-550, 558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 14-25

Cell attachment sequence: amino acids 247-250

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FIGURE 121

[illegible]

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FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
 FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ
 EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNIATLEDCAIMRDSS
 NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence: amino acids 1-42

N-glycosylation site: amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site: amino acids 51-55,
 120-124, 163-167, 175-179, 181-185

N-myristoylation site: amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 27-38

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FIGURE 123A

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGG
CGGCCACCGCGACTCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCCTGCTGCTGCTTTTCAG
GGGCTGCCTGATAGGGGCTGTAAATCTCAAATCCAGCAATCGAACCCCAGTGGTACAGGAAT
TTGAAAGTGTGGAAGTGTCTTGCATCATTACGGATTTCGCAGACAAGTGACCCCAGGATCGAG
TGGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTTTTGACAACAAAATTTCAGGGAGA
CTTGCGGGTTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGA
GAGACTCAGCCCTTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGCAAGGAAATTGATGAG
ATTGTGATCGAGTTAACTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGC
TGTACCAGTAGGCAAGATGGCAACACTGCACTGCCAGGAGAGTGAGGGCCACCCCCGGCCTC
ACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATTCCAGAGCCAATCCCAGATTT
CGCAATTCTTCTTTCCACTTAACTCTGAAACAGGCACTTTGGTGTTCACTGCTGTTACAA
GGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGG
AGCAGGAGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGGTTGTC
CTTGCTGTACTGGCCCTGATCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCAT
CAACAATAAACAGGATGGAGAAAGTTACAAGAACCCAGGGAAACCAGATGGAGTTAACTACA
TCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTGTGATCTGAGACCCGCGG
TGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAAGGCA
GCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTTGGCCAA
AGTTGACCACTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCCTCAAGATG
GACCCGGTAAATATAACCACAAGGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCCTAA
TCTGTTTTCTGGCCTGATTCCCGCATGAGTATTAGGGTGATCTTAAAGAGTTTGCTCACGTAA
ACGCCCGTGCTGGGCCCTGTGAAGCCAGCATGTTACCACTGGTCGTTACGAGCCACGACA
GCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGGCGGGAACCCAG
AAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCT
TAAAGGCTCTGCTGATCGGTGTTGCAGTGTCCATTGTGGAGAAGCTTTTTGGATCAGCATTT
TGTA AAAACAACCAAAATCAGGAAGGTAAATTGGTTGCTGGAAGAGGGATCTTGCCTGAGGA
ACCCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAAACCTTCGTCTTAGGCTAAGTCTGA
AATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTTTACATCTAAAT
TTTTGCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAACTGTAAATATATT
GTCATACAATGTTAAATAACCTATTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAG
CTACTAGTGTTAAATTGGAAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCA

To Figure 123B

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FIGURE 123B

From Figure 123A

TGGAAGTTTACTGTGATGTTTCCTTTTCTCACACAAGTTTTCAGCCTTTTTCACAAGGGAACTC
ATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTTTAAAAATTCCAGTTAAGCAAT
GTTGAAATCAGTTTGCATCTCTTCAAAGAAACCTCTCAGGTTAGCTTTGAACTGCCTCTTC
CTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACAC
AGATGCCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCCGCTCTAGCTCACTGTTGCCTCGC
TGTCTGCCAGGAGGCCCTGCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCCAGTGAGCTTTA
CTCACGTGGCCCTTGCTTCATCCAGCACAGCTCTCAGGTGGGCACTGCAGGGACACTGGTGT
CTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAACAGACCTCTTTTTGGTTATGGATGGCT
CACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTTAAAGTTTGTTTAATTATTTGTTAAGAT
TGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTAAAAGA
AAATGGATCCCAGTGTTCCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGC
CATTTCAAACAAACCATGATGGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTCAGGTGG
AGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAGTGAAACGCCTGAATCAAAGCAGTTTTTC
TAATTTTGACTTTAAATTTTTCATCCGCCGAGACACTGCTCCCATTGTGGGGGGACATTA
GCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCTGC
CGTGCTGGACTCAGGACTGAAGTGCTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACT
GTGTGCCTGGAGAATGGCTCTCACTACTCACCTTGTCTTTCAGCTTCCAGTGTCTTGGGTTT
TTTATACTTTGACAGCTTTTTTTTAAATTGCATACATGAGACTGTGTTGACTTTTTTTAGTTA
TGTGAAACACTTTGCCGCAGGCCCGCTGGCAGAGGCAGGAAATGCTCCAGCAGTGGCTCAGT
GCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTCCTCCATCATTG
CCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACGCTCCAGCCTCC
TTCTTGGTTGTCATAGTGATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCCTAAAACCTT
CTACACTAGTGCCATGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAAGTAGAGTCTGGG
AAGTAGCTGCCTATAACTGAGACTAGACGGAAAAGGAATACTCGTGTATTTTAAGATATGAA
TGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCTGCCTTTGGATGGATGTTGCTGT
ACACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTGTGTTAACCTCATTTAT
AAAAGCTTCAAAAAAACCCA

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FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
 PRIEWKKIQDEQTTYVFFDNKIQGDLGRAEILGKTSCLKIWNVTRRDSALYRCEVVARNDRK
 EIDEIVIELTVQVKPVPVCRVPAKVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
 NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDNLNIGGIIGG
 VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Signal peptide: amino acids 1-30

Transmembrane domain: amino acids 243-263

N-glycosylation sites: amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 amino acids 107-110

Casein kinase II phosphorylation site: amino acids 106-109,
 296-299

Tyrosine kinase phosphorylation site: amino acids 69-77

N-myristoylation sites: amino acids 26-31, 215-220, 226-231,
 243-248, 244-249, 262-267